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OM nucleic - nucleic search, using sw model  
Run on: July 21, 2000, 01:57:46 ; Search time 2513.97 Seconds  
(without alignments)  
705.652 Million cell updates/sec

Title: US-09-016-869A-1  
Perfect score: 994  
Sequence: 1 CGGAGAGGGGAGACAGAC.....CATTCACTCACTCAAAAAA 994

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 972840 seqs, 892348106 residues 1945680  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 1000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_bal.\*
- 2: gb\_ba2.\*
- 3: gb\_om.\*
- 4: gb\_ov.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
- 9: gb\_pr1.\*
- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sts.\*
- 14: gb\_sy.\*
- 15: gb\_un.\*
- 16: em\_fun.\*
- 17: em\_hum1.\*
- 18: em\_hum2.\*
- 19: em\_in.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_sy.\*
- 29: em\_un.\*
- 30: em\_vi.\*
- 31: gb\_htg1.\*
- 32: gb\_htg2.\*
- 33: gb\_in1.\*
- 34: gb\_in2.\*
- 35: em\_ba1.\*
- 36: em\_ba2.\*
- 37: em\_hum3.\*
- 38: em\_hum4.\*
- 39: gb\_pr4.\*
- 40: gb\_htg3.\*
- 41: gb\_htg4.\*
- 42: gb\_htg5.\*
- 43: gb\_htg6.\*

- 44: gb\_htg7.\*
- 45: em\_htg1.\*
- 46: em\_htg2.\*
- 47: em\_htg3.\*
- 48: em\_hum5.\*
- 49: gb\_pl3.\*
- 50: gb\_pr5.\*
- 51: gb\_htg8.\*
- 52: gb\_htg9.\*
- 53: gb\_htg10.\*
- 54: gb\_htg11.\*
- 55: gb\_htg12.\*
- 56: gb\_htg13.\*
- 57: gb\_htg14.\*
- 58: gb\_in3.\*
- 59: gb\_htg15.\*
- 60: gb\_htg16.\*
- 61: gb\_htg17.\*
- 62: em\_htg4.\*
- 63: em\_htg5.\*
- 64: em\_htg6.\*
- 65: em\_htg7.\*
- 66: em\_hum6.\*
- 67: gb\_htg18.\*
- 68: gb\_htg19.\*
- 69: gb\_htg20.\*
- 70: gb\_htg21.\*
- 71: gb\_htg22.\*
- 72: gb\_htg23.\*
- 73: gb\_htg24.\*
- 74: gb\_htg25.\*
- 75: gb\_htg26.\*
- 76: gb\_htg27.\*
- 77: gb\_htg28.\*
- 78: gb\_htg29.\*
- 79: gb\_htg30.\*
- 80: gb\_htg31.\*
- 81: gb\_vil.\*
- 82: gb\_vil2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	982.2	98.8	987	10	HUMINK4X	L27211 Human CDK4-
	2	943.8	94.9	947	5	AR001346	AR001346 Sequence
	3	943.8	94.9	947	5	AR037526	AR037526 Sequence
	4	943.8	94.9	947	5	AR062806	AR062806 Sequence
	5	943.8	94.9	947	5	I41180	I41180 Sequence 36
	6	801	80.6	1017	10	HSU26727	U26727 Human p16IN
	7	801	80.6	1131	5	AR001325	AR001325 Sequence
	8	801	80.6	1131	5	AR037505	AR037505 Sequence
	9	801	80.6	1131	5	AR062785	AR062785 Sequence
	10	801	80.6	1131	5	I41159	I41159 Sequence 13
	11	705.4	71.0	1420	5	I67718	I67718 Sequence 1
	12	551.2	55.5	905	10	HSU38945	U38945 Human hypot
	13	489.2	49.2	520	39	S69822S2	S69824 Homo sapien
C	14	489.2	49.2	34669	39	AC000048	AC000048 Homo sapi
	15	467.8	47.1	471	5	AR001314	AR001314 Sequence
	16	467.8	47.1	471	5	AR037494	AR037494 Sequence
	17	467.8	47.1	471	5	AR062774	AR062774 Sequence
	18	467.8	47.1	471	5	I41148	I41148 Sequence 1
	19	379	38.1	400	13	GI3475	GI3475 human STS S
	20	358.6	36.1	793	39	AF115544	AF115544 Homo sapi
	21	330	33.2	660	11	S78535	S78535 tumor suppr
	22	310.4	31.2	457	39	S69804	S69804 MTS1-multipli
	23	310.4	31.2	540	39	S69822S1	S69822 Homo sapien
	24	310.4	31.2	1187	5	AR001316	AR001316 Sequence







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Db 361 CTGGGCATCGCATGTCGACAGGTACCTGCGCGGGCTGCGGGGGGCACACAGAGGAGT 420  
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QY 461 AACCATGCCCGCATAGATGCGCGGAAGTTCCTCAGACATGCTCCCGCTTGAAGAACCCAG 520  
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QY 521 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGTCACCAAGAGTCTACAGGGCC 580  
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Db 481 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGTCACCAAGAGTCTACAGGGCC 540  
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QY 581 ACAACTGCCCGCCGACCAACCCCGCTTTCGTAGTTCATTTAGAAAAATAGAGCTT 640  
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Db 541 ACAACTGCCCGCCGACCAACCCCGCTTTCGTAGTTCATTTAGAAAAATAGAGCTT 600  
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QY 641 TTAATAATGCTTCCCTTTTAAAGTATATAGCTTACCGCTTCCCGCTTGAAGAACCCAG 700  
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QY 701 TTTATATCATTTTATATATTTTATATAATGTAATAAATGTAATAAAGAAACACCGCTTCTGCC 760  
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QY 761 TTTTCACTGTGTGGAGTTTCTGGAGTGAGCAGTACACGCTTCAAGCGCACATTTCTGTG 820  
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QY 821 GGCATTTCTTGGAGCTCGAGCTTCCGGAAGTTCCTGAGTTCATTTAGAAAAATAGAGCTT 880  
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Db 781 GGCATTTCTTGGAGCTCGAGCTTCCGGAAGTTCCTGAGTTCATTTAGAAAAATAGAGCTT 840  
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QY 881 GAACCTAGGAGCTCAGGGGGTCTACTGGCTTCTTGTAGTTCATTTCAATTCATTCACCTC 940  
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Db 901 AGAACCAAGCTCAATAAAAAATTAATAATTTTCAATTCATTCACCTC 987  
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RESULT 4  
AR062806 207 a 271 c 274 g 195 t  
LOCUS AR062806 947 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 36 from patent US 5843756.  
ACCESSION AR062806  
VERSION AR062806.1 GI:5990497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Stone,S., Jiang,P. and Kamb,A.  
TITLE Mouse MTSI gene  
JOURNAL Patent: US 5843756-A 36 01-DEC-1998;  
FEATURES  
source Location/Qualifiers  
1. .947  
BASE COUNT 207 a 271 c 274 g 195 t  
ORIGIN  
Query Match 94.9%; Score 943.8; DB 5; Length 947;  
Best Local Similarity 99.8%; Pred. No. 7.3e-151;  
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 101 GCCCGGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGGTGCTGCTGCCAACGCA 160  
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QY 161 CCGAATAGTTACGGTCGGAGGCGGATCCAGGTTCATGATGGGAGCGCGGAGTGGCG 220  
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Db 121 CCGAATAGTTACGGTCGGAGGCGGATCCAGGTTCATGATGGGAGCGCGGAGTGGCG 180  
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Db 181 GAGTCTGCTGCTGCTCACGGCGGAGCCAACTGCGCCGACCCCGCCACTCTCACCCGA 240  
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QY 281 CCGTGCACGAGCTGCCCGGAGGGCTTCTTGGACACGCTGGTGGTGTGACCGGGCC 340  
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Db 241 CCGTGCACGAGCTGCCCGGAGGGCTTCTTGGACACGCTGGTGGTGTGACCGGGCC 300  
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Db 301 GGGGCGGGCTGAGCTGCGCGATGCTGGGCGGCTCTGCGGTGACCTGGCTGAGGAG 360  
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Db 481 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGTCACCAAGAGTTCCTACAGGGCC 540  
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QY 581 ACAACTGCCCGCCGACCAACCCCGCTTTCGTAGTTCATTTAGAAAAATAGAGCTT 640  
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Db 601 TTAATAATGCTTCCCTTTTAAAGTATATAGCTTCCCGCTTGAAGAACCCAG 660  
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QY 701 TTTATATCATTTTATATATTTTATATAATGTAATAAATGTAATAAAGAAACACCGCTTCTGCC 760  
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Db 661 TTTATATCATTTTATATATTTTATATAATGTAATAAATGTAATAAAGAAACACCGCTTCTGCC 720  
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QY 941 AGAACCAAGCTCAATAAAAAATTAATAATTTTCAATTCATTCACCTC 987  
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Db 901 AGAACCAAGCTCAATAAAAAATTAATAATTTTCAATTCATTCACCTC 947  
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RESULT 5  
I41180 947 bp DNA PAT 13-MAY-1997  
LOCUS I41180  
DEFINITION Sequence 36 from patent US 5624819.  
ACCESSION I41180  
VERSION I41180.1 GI:2081770  
KEYWORDS  
SOURCE Unknown.







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Db 991 CCGGAAGCTGTCGACTTCATGACAAAGCATTTTGTGAAGCTAGGAAAGCTCAGGGGGTTAC 1050
Qy 907 TGGCTTCTCTTGAGTCACACTGCTAGCAATAGCGAGAACCAAGCTCAAAATAAAATAAA 966
Db 1051 TGGCTTCTCTTGAGTCACACTGCTAGCAATAGCGAGAACCAAGCTCAAAATAAAATAAA 1110
Qy 967 ATTATTTTCATTCATTCACCTC 987
Db 1111 ATTATTTTCATTCATTCACCTC 1131

RESULT 10
LOCUS I41159 1131 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 13 from patent US 5624819.
ACCESSION I41159
VERSION I41159.1 GI:2081749
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1131)
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Germ-line mutations in the MTS gene
JOURNAL Patent: US 5624819-A 13 29-APR-1997;
FEATURES Location/Qualifiers
source 1..1131
BASE COUNT 232 a 327 c 343 g 229 t
ORIGIN

Query Match 80.6%; Score 801; DB 5; Length 1131;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 CCAGTCATGATGATGGGAGCGCCGAGTGGCGAGCTGCTGCTCCAGGCGCGGA 246
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Db 391 GCCCAACTGCGCGACCGCCGACATCTACCCGACCGGTCGACGACGCTGCCCGGAGGG 450
Qy 307 CTTCTGGACACGCTGGTGGTCTGCACCGGCGCGGGCTGGACGTCGCGCATGC 366
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Qy 367 CTGGGCGGCTCTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCGGATGTCGACGGTA 426
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Qy 427 CTTGCGCGGCTGCGGGGGGACAGAGGCTTAACATGCTCCGATAGTCCGCGGA 486
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Qy 667 GATATAAGCTTCCCGCCACTACCGTAAATGTCCATTTATATATATATATATATATAT 726
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Db 1111 ATTATTTTCATTCATTCACCTC 1131

RESULT 11
LOCUS I67718 1420 bp DNA PAT 30-DEC-1997
DEFINITION Sequence 1 from patent US 5672508.
ACCESSION I67718
VERSION I67718.1 GI:2731253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1420)
AUTHORS Gyuris,J., Lamphere,L. and Beach,D.
TITLE Inhibitors of cell-cycle progression, and uses related thereto
JOURNAL Patent: US 5672508-A 1 30-SEP-1997;
FEATURES Location/Qualifiers
source 1..1420
BASE COUNT 322 a 410 c 458 g 230 t
ORIGIN

Query Match 71.0%; Score 705.4; DB 5; Length 1420;
Best Local Similarity 99.2%; Pred. No. 1.9e-110;
Matches 709; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 32 GGGAGCAGCATGGATCCGCGCGGGGAGCAGCATGGAGCCTTCGGGCTGACTGGCTGGCC 91
Db 700 GGGAGCAGCATGGAGCGGCGGGGAGCAGCATGGAGCCTTCGGGCTGACTGGCTGGCC 759
Qy 92 ACGGCGCGGCGCGGGTCTGGGTAGAGAGTGGCGGCGCTGCTGGAGGCGGTGGCGCTG 151
Db 760 ACGGCGCGGCGCGGGTCTGGGTAGAGAGTGGCGGCGCTGCTGGAGGCGGTGGCGCTG 819
Qy 152 CCCAACGACCAATAGTTACGGTCGGAGCGCGATCCAGGTCATCATGATGGGAGCGCC 211
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Qy 212 CGAGTGGCGGAGCTGCTGCTCTCCAGCGCGGAGCCAACTGCGGACCCGCGCACT 271
Db 880 CGAGTGGCGGAGCTGCTGCTCTCCAGCGCGGAGCCAACTGCGGACCCGCGCACT 939
Qy 272 CTCACCGGACCCGTCGACGACGCTGCGCGGAGGGCTTCCTGGACACGCTGGTGGTGTG 331
Db 940 CTCACCGGACCCGTCGACGACGCTGCGCGGAGGGCTTCCTGGACACGCTGGTGGTGTG 999
Qy 332 CACCGGCGCGGCGCGGCTGAGCTGCGCGATCGCTGGGCGCTCTGCGCGCTGAGACCTG 391
Db 1000 CACCGGCGCGGCGCGGCTGAGCTGCGCGATCGCTGGGCGCTCTGCGCGCTGAGACCTG 1059
Qy 392 GCTGAGGAGCTGGGCGCATTCGCGAGTGTGCGACGGTACCTGCGCGGGGCTGCGGGGGACC 451
Db 1060 GCTGAGGAGCTGGGCGCATTCGCGAGTGTGCGACGGTACCTGCGCGGGGCTGCGGGGGACC 1119
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QY 632 ATAGAGCTTTTAAATGTCCTGCTTTTAAAGTAGATATAAGCTTCCGCCACTACCT 591
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RESULT 12
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LOCUS HSU38945 905 bp mRNA PRI 05-JUN-1996
DEFINITION Human hypothetical 18.1 kDa protein (CDKN2A) mRNA, complete cds.
ACCESSION U38945
VERSION U38945.1 GI:1353569
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Linnenbach,A.J.
TITLE mRNA isoform with alternate first exon-encoded sequences at the
cyclin-dependent kinase inhibitor 2 (p16INK4/MTS1) locus and
mapping analysis of the region by using long-PCR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 905)
AUTHORS Linnenbach,A.J.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1995) Alban J. Linnenbach, The Wistar Institute,
3601 Spruce Street, Philadelphia, PA 19104, USA
FEATURES
location/Qualifiers
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38..559
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reading frame"
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BASE COUNT 168 a 272 c 299 g 166 t
ORIGIN
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Query Match 55.5%; Score 551.2; DB 10; Length 905;
Best Local Similarity 99.5%; Pred. No. 2.7e-84;
Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 487 AGTCCCTCAGACATCCCGGATTGAAAGAACGAGAGAGGCTCTGAGAAACCTCGGGAAAC 546
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QY 547 TTAGATCATCATCAGTACCGAAGTCTTACAGGCGCCACAACTGCCCGCCACACCCACCC 606
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Db 710 TTAGATCATCATCAGTACCGAAGTCTTACAGGCGCCACAACTGCCCGCCACACCCACCC 769
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QY 607 CGCTTTCGTAGTTTTCATTAGAAAATAGAGCTTTTAAATAATGCTCGCTCTTTACGTA 666
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RESULT 13
S69822S2
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DEFINITION Homo sapiens CDK4i exon, partial sequence; and cyclin-dependent
kinase 4 inhibitor (CDK4i) gene, partial cds.
ACCESSION S69824
VERSION S69824.1 GI:546701
KEYWORDS
SEGMENT 2 of 2
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Nobori,T., Miura,K., Wu,D.J., Lois,A., Takabayashi,K. and
Carson,D.A.
TITLE Deletions of the cyclin-dependent kinase-4 inhibitor gene in
multiple human cancers
JOURNAL Nature 368 (6473), 753-756 (1994)
MEDLINE 94203288
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 146822] from the original journal article.
FEATURES
Location/Qualifiers
1..520
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="melanoma"
source
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AUTHORS	Sween,L., Olopade,F.I. and Rowley,J.D.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 34669)
AUTHORS	Burian,D.M., Mitchell,N. and Roe,B.A.
TITLE	Homo sapiens Cosmid Clone c66 encoding the p16/CDK-INK4 gene
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 34669)
AUTHORS	Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (30-OCT-1996) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE	4 (bases 1 to 34669)
AUTHORS	Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
COMMENT	On Sep 15, 1999 this sequence version replaced gi:5801678.
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Best Local Similarity	99.4%; Pred. No. 7.4e-74;
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Db 22159	CAGACATCCCAGATTGAAAGAACACAGAGAGGCTCTGAGAAACCTCGGGAACCTTAGATCA 22100
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Db 22099	TCAGTCACCGAAGGTCCTACAGGGCCACAACCTGCCCGCCGACACACCCCGCTTTCG 22040
QY 615	TAGTTTTTCATTAGAAAATAGAGCTTTTAAAAATGCTCTGCTCTTTTAAGCTAGATATAAG 674
Db 22039	TAGTTTTTCATTAGAAAATAGAGCTTTTAAAAATGCTCTGCTCTTTTAAGCTAGATATAG 21980
QY 675	CTTCCCGCCACTACCGTAAATGTCCATTATATATATTTTATATATCTTTATAAAATG 734
Db 21979	CTTCCCGCCACTACCGTAAATGTCCATTATATATATTTTATATATCTTTATAAAATG 21920
QY 735	TAAAAAGAAAACACCGCTTCGCTTTTCACCTGTTGGAGTTTCTGGAGTGAGCAC 794
Db 21919	TAAAAAGAAAACACCGCTTCGCTTTTCACCTGTTGGAGTTTCTGGAGTGAGCAC 21860
QY 795	TCAGGCCCTAAGCGCACATTCATGTGGCATTTCTTTGGAGCCTCGCAGCCCTCCGGAAGC 854
Db 21859	TCAGGCCCTAAGCGCACATTCATGTGGCATTTCTTTGGAGCCTCGCAGCCCTCCGGAAGC 21800
QY 855	TGTGACTTCATGACAGCATTTTGTGAACCTAGGGAAGCTCAGGGGGGTACTGGCTTCT 914
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QY 915	CTTGAGTCACACTGCTAGCAATGGCAACCCAAAGCTCAAAATAAAAAATAAATATTTT 974
Db 21739	CTTGAGTCACACTGCTAGCAATGGCAACCCAAAGCTCAAAATAAAAAATAAATATTTT 21680
QY 975	CATTCAATCACTCA 988
Db 21679	CATTCAATCACTCA 21666



RESULT 15  
AR001314 AR001314 471 bp DNA PAT 04-DEC-1998  
LOCUS Sequence 1 from patent US 5739027.  
DEFINITION AR001314  
ACCESSION AR001314  
VERSION AR001314.1 GI:3963381  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Kamb,A.  
TITLE MTS1E1.beta.gene  
JOURNAL Patent: US 5739027-A 1 14-APR-1998;  
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source  
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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 3.8e-70;  
Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 GCCCGGGTTCGGGTAGAGAGGTGGGGGGCTGCTGGAGCGCGGGCGCTGCCCAACGCA 120  
QY 161 CCGAATAGTACGGTCGGAGCGCATCCAGGTCAATGATGGGAGCGCCCGAGTGGCG 220  
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QY 221 GAGCTGCTGCTCTCCACGGCGGGAGCCCAACTGGCGGACCCCGCCACTCTCACCCGA 280  
Db 181 GAGCTGCTGCTCTCCACGGCGGGAGCCCAACTGGCGGACCCCGCCACTCTCACCCGA 240  
QY 281 CCGGTGACGAGCGTGCCTGGGGAGGGCTTCCTGGACACGCTGGTGGTGCACCGGGCC 340  
Db 241 CCGGTGACGAGCGTGCCTGGGGAGGGCTTCCTGGACACGCTGGTGGTGCACCGGGCC 300  
QY 341 GGGGCGCGGCTGGACGTGCGCGATGCCCTGGGCCCTCTGCCCGTGGACCTGGCTGAGGAG 400  
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QY 401 CTGGGCGCATCGCGNTGTCCACGAGTACCTGGCGGGGCTGGCGGGGGACACAGAGGCAGT 460  
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QY 461 AACCATGCCCGCATAGATCCCGGAAGGTCCCTCAGACATCCCGATTGA 511  
Db 421 AACCATGCCCGCATAGATCCCGGAAGGTCCCTCAGACATCCCGATTGA 471



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_36:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	994	100.0	994	1	T02962	Cell-cycle regulat
2	982.2	98.8	987	1	T60951	Tumour suppressor
3	945.4	95.1	947	1	T00747	Multiple tumour su
4	943.8	94.9	947	1	T72311	Human multiple tum
5	943.8	94.9	947	1	V11270	Human MTS1 cDNA va
6	943.8	94.9	947	1	V53851	Coding sequence 3
7	943.8	94.9	947	1	V70615	cDNA encoding a hu
8	937.6	94.3	948	1	Q63491	Inhibitor of cycli
9	801	80.6	1131	1	T00744	Multiple tumour su
10	801	80.6	1131	1	Q99164	Human MTS polypt
11	801	80.6	1131	1	T69780	Human multiple tum
12	801	80.6	1131	1	V11249	Human MTS1E1-beta
13	801	80.6	1131	1	V53830	Coding sequence 1
14	801	80.6	1131	1	V70594	cDNA encoding a hu
15	705.4	71.0	1420	1	T74051	CDK inhibitory fus
16	705.4	71.0	1420	1	T26220	Human p27-p16 fus
17	489.2	49.2	4866	1	T13158	CDK41 cyclin-depen
18	468.8	47.2	782	1	X26234	Truncated p27/p16
19	468.8	47.2	1073	1	X26232	Truncated p27/p16
20	467.8	47.1	471	1	V11238	Human MTS1 cDNA. D
21	467.8	47.1	471	1	V53819	Nucleotide sequenc
22	467.8	47.1	471	1	V70583	cDNA encoding a hu
23	467.4	47.0	737	1	X26233	Truncated p27/p16
24	467.4	47.0	1028	1	X26231	Truncated p27/p16
25	467.4	47.0	1121	1	X26235	Human p16p27 fusio
26	466.2	46.9	471	1	T69768	Human multiple tum
27	466.2	46.9	471	1	T69769	Human multiple tum
28	463.8	46.7	1143	1	T74052	CDK inhibitory fus
29	463.8	46.7	1143	1	X26223	Human p16(GS)p27 f
30	463.4	46.6	1098	1	T74053	CDK inhibitory fus
31	463.4	46.6	1098	1	X26224	Human p16p27 fusio
32	447	45.0	447	1	T00736	Multiple tumour su
33	447	45.0	447	1	Q99158	Human multiple tum

## ALIGNMENTS

RESULT	1
T02962	
ID	T02962 standard; cDNA; 994 BP.
AC	T02962;
DT	01-MAR-1996 (first entry)
DE	Cell-cycle regulatory protein p16 cDNA.
KW	Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
KW	CCR; gene therapy; transgenic animal; cancer; cell proliferation;
KW	ss; ds.
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	cds 41..511
FT	/tag= a
FN	WO9528483-A1.
PD	26-OCT-1995.
PF	14-APR-1995; U04635.
PR	14-APR-1994; US-227371.
PR	25-MAY-1994; US-248812.
PR	14-SEP-1994; US-306511.
PR	29-NOV-1994; US-346147.
PA	(COLD-) COLD SPRING HARBOR LAB.
PI	Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR	WFI: 95-373798/48.
DR	P-FSDB; R85116.
PT	New cell cycle regulating proteins bind to cyclin dependent kinase -
PT	and related nucleic acids, antibodies etc., used in diagnosis and
PT	therapy of abnormal cell proliferation, degeneration etc.
PS	Claim 43: Page 76-77; 109pp; English.
CC	cDNA (T02962) coding for the human cell-cycle regulatory (CCR)
CC	protein p16 (R85116) was isolated using a 2-hybrid screening assay
CC	in Saccharomyces cerevisiae. The p16 gene was mapped to chromosome
CC	9p21-22. The isolated cDNA can be used: to detect mutations in
CC	CCR genes that lead to cell proliferation; to breed transgenic
CC	animals to study cellular disorders involving CCR allele
CC	mutation/misexpression; and to correct CCR-deficient cells
CC	(gene therapy).
SQ	Sequence 994 BP; 225 A; 279 C; 293 G; 197 T;
Query Match	100.0%; Score 994; DB 1; Length 994;
Best Local Similarity	100.0%; Pred. No. 2.3e-214;
Matches 994; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY	181 GCCGATCCAGGTGATGATGATGGCAGCGCCCGGAGTGCGTGCTCTCCAGCG 240 

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Qy 301 GGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGGCGCGGCGCTGGAGCTGCG 360
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Qy 361 CGATGCTGGGCGCTGCGCGTGGAGCTGCTGAGAGCTGGGCGATGCGGATGTCG 420
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Db 541 GGAACCTTAGATCATCAGTACCGAGGCTCTACAGGGCCACACTGCCCCGCCACAA 600
Qy 601 CCACCCCGCTTCGTTAGTTTTCATTAGAAATAGAGCTTTTAAATGTCTGCTTTT 660
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Qy 721 TTCTTATAAATGTAAGAAAGAAACACGCTCTGCTTTTACATGTTGAGTTT 780
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Qy 841 CAGCCTCGGAAGCTGTCGACTTCATGACAGCATTTTGTGAAGTGGAGCTCAGGG 900
Db 841 CAGCCTCGGAAGCTGTCGACTTCATGACAGCATTTTGTGAAGTGGAGCTCAGGG 900
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Qy 961 AATAAATTTTTCATTCTACTCAAAAAA 994
Db 961 AATAAATTTTTCATTCTACTCAAAAAA 994

RESULT 2
ID T60951 standard; DNA; 987 BP.
AC T60951;
DT 28-OCT-1997 (first entry)
DE Tumour suppressor p16 coding sequence.
KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;
KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
KW anti-angiogenic activity; hyperproliferative disorder; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 41..511
FT /*tag= a
FT /product= Tumour suppressor p16
FN WO9703635-A2.
PD 06-FEB-1997.
PF 17-JUL-1996; U11787.
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```
PR 17-JUL-1995; US-502881.
PA (TEXA ) UNIV TEXAS SYSTEM.
PI Jin X, Roth J;
DR WPI; 97-132336/12.
DR P-PSDB: W10627.
PT Expression construct contg. DNA for tumour suppressor p16 - to
PT restore p16 activity to transformed cells, useful for treating lung
PT or bladder cancer or melanoma
PS Disclosure; Fig 1a; 92pp; English.
CC This sequence represents the coding sequence for the tumour suppressor
CC p16. This sequence is joined to a promoter functional in eukaryotic cells
CC and used in the expression construct of the invention. p16 is an
CC inhibitory subunit, which is involved in the control of cyclin-dependent
CC kinase 4 activity, and functions as a tumour suppressor. By detecting
CC this sequence or the encoded protein, cancer cells can be detected. When
CC the nucleic acid molecule is in the sense orientation, the expression
CC construct can be used to restore p16 function in a cell, particularly by
CC reversing the transformed phenotype in tumours, especially lung or
CC bladder cancer or melanoma. It may also have anti-angiogenic activity,
CC and inhibit hyperproliferative disorders, e.g. restenosis. When the
CC nucleic acid molecule is inserted in the antisense orientation, the
CC expression construct inhibits p16 function. Reduced or increased levels
CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
CC or immunoassay.
SQ Sequence 987 BP; 219 A; 279 C; 295 G; 194 T;

Query Match 98.8%; Score 982.2; DB 1; Length 987;
Best Local Similarity 99.7%; Pred. No. 1e-211; 3; Indels 0; Gaps 0;
Matches 984; Conservative 0; Mismatches 3;

Qy 1 CGGAGAGGGGAGAACAGACAGCGGGGGGAGCAGCAGTGGATCCGCGCGGGGAG 60
Db 1 CGGAGAGGGGAGAACAGACAGCGGGGGGAGCAGCAGTGGATCCGCGCGGGGAG 60
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Db 61 CAGCATGGAGGCTTCGCTGACTGGCTGGCCACGCGCGCGGGTGGGTAGAGGA 120
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Qy 181 GCCGATCCAGGTCAATGATGATGGGACGCGCCCGAGTGGCGAGCTGCTGTCTCCACGG 240
Db 181 GCCGATCCAGGTCAATGATGATGGGACGCGCCCGAGTGGCGAGCTGCTGTCTCCACGG 240
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Db 541 GGAACCTTAGATCATCAGTACCGAGGCTCTACAGGGCCACAACTGCCCCGCCACAA 600
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Db 601 CCACCCCGCTTGGTATTTTCAATTTAGAAATAGAGCTTTTAAATATGCTCGCCTTTT 560  
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Qy 721 TTCTTTAAATATGTAAGAAAGAAACACCGCTTCTGCTTTTCACTGTGTGAGTTT 780  
Db 721 TTCTTTAAATATGTAAGAAAGAAACACCGCTTCTGCTTTTCACTGTGTGAGTTT 780  
Qy 781 TCTGGAGTGAGCACTCACGCCCTAACGCGACATTCATGTGGGCAATTTCTTGGAGCCTCG 840  
Db 781 TCTGGAGTGAGCACTCACGCCCTAACGCGACATTCATGTGGGCAATTTCTTGGAGCCTCG 840  
Qy 841 CAGCCTCCGGAAGCTGTCGACTTTCATGACAAGCATTTTGTGAAGTGGGAAAGCTCAGGGG 900  
Db 841 CAGCCTCCGGAAGCTGTCGACTTTCATGACAAGCATTTTGTGAAGTGGGAAAGCTCAGGGG 900  
Qy 901 GGTACTGCTTCTTGTAGTCACACTGCTAGCAATGCGAGAACCAAGCTCAATATAA 960  
Db 901 GGTACTGCTTCTTGTAGTCACACTGCTAGCAATGCGAGAACCAAGCTCAATATAA 960  
Qy 961 ATATAAATATTTTCAATTCATTCACCTC 987  
Db 961 ATATAAATATTTTCAATTCATTCACCTC 987

RESULT 3

T00747  
ID T00747 standard; cDNA; 947 BP.  
AC T00747;  
DT 08-MAY-1996 (first entry)  
DE Multiple tumour suppressor 1 (MTS1) cDNA.  
KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;  
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;  
KW pancreas; breast; thyroid; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT misc\_feature 151  
FT /\*tag= a  
FT /\*note= "splice site acceptor"  
FT 458  
FT /\*tag= b  
FT /\*note= "splice site acceptor"  
FT  
PN WO9525013-A1.  
PD 28-SEP-1995.  
PF 17-MAR-1995; U03537.  
PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215087.  
PR 18-MAR-1994; US-215086.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (UTAH) UNIV UTAH RES FOUND.  
PI Cannon-Albright LA, Kamb A, Skolnick MH;  
DR WPI: 95-344626/44.  
PT Detecting polymorphism associated with cancer pre-disposition - also  
PT DNA, vectors and host cells e.g. for gene or protein replacement  
PT therapy and drug screening  
PS Disclosure; Pages 111-112; 148pp; English.  
CC An individual can be diagnosed as having a predisposition to cancer  
CC by detecting an alteration in the wild type multiple tumour  
CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1  
CC cDNA T00747. The above assay can also be used in the diagnosis and  
CC prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and  
CC thyroid cancers, etc.  
SQ Sequence 947 BP; 207 A; 271 C; 273 G; 196 T;

Query Match 95.1%; Score 945.4; DB 1; Length 947;  
Best Local Similarity 99.9%; Pred. No. 1.8e-203;  
Matches 946; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ATGGAGCGCGCGCGGGGAGAGCATGAGAGCTTCGGGCTGACTGCTGCGCACGCCCGCG 60  
Qy 101 GCCCGGGTTCGGGTAGAGAGGTGCGGCGCTGCTGAGGCGGTGCGCTGCCAACGCA 160  
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Qy 161 CGGAATAGTTACGGTTCGGAGCGCGATCCAGGTTCATGATGGGAGGCGCGCGAGTGGCG 220  
Db 121 CGGAATAGTTACGGTTCGGAGCGCGATCCAGGTTCATGATGGGAGGCGCGCGAGTGGCG 180  
Qy 221 GAGCTGTGCTGCTCCACGCGCGGAGCCCAACTGCGCGGACCCGCCCACTCTCACCGA 280  
Db 181 GAGCTGTGCTGCTCCACGCGCGGAGCCCAACTGCGCGGACCCGCCCACTCTCACCGA 240  
Qy 281 CCCGTGCAGGAGCGCTCCCGGGAGGGCTTCCTGGACACGCTGCTGCTGACCGGGCC 340  
Db 241 CCCGTGCAGGAGCGCTCCCGGGAGGGCTTCCTGGACACGCTGCTGCTGACCGGGCC 300  
Qy 341 GGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTTCTGCCGCTGGAGCTGCTGAGGAG 400  
Db 301 GGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTTCTGCCGCTGGAGCTGCTGAGGAG 360  
Qy 401 CTGGGCGCATCGGATGCTGCGACGGTACCTGCGCGGGCTGCGGGGGGACACAGAGCAGT 460  
Db 361 CTGGGCGCATCGGATGCTGCGACGGTACCTGCGCGGGCTGCGGGGGGACACAGAGCAGT 420  
Qy 461 AACCATGCCGATAGATGCCGGAAGTCCCTCAGACATCCCGATTGGAAGAACAG 520  
Db 421 AACCATGCCGATAGATGCCGGAAGTCCCTCAGACATCCCGATTGGAAGAACAG 480  
Qy 521 AGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCAGTACCGAAGTCTCTACAGGGCC 580  
Db 481 AGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCAGTACCGAAGTCTCTACAGGGCC 540  
Qy 581 ACACTGCGCGCGCGCACAAACCCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 640  
Db 541 ACACTGCGCGCGCGCACAAACCCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 600  
Qy 641 TTAATAATGCTGCTGCTTTTAACTAGATATAGAGCTTCCCGCCACTACCGTAAATGTCCA 700  
Db 601 TTAATAATGCTGCTGCTTTTAACTAGATATAGAGCTTCCCGCCACTACCGTAAATGTCCA 560  
Qy 701 TTTATATCATTTTTTATATATTTTATATAATGTAATAAAGAAAAACACCCCTTCTGCC 760  
Db 661 TTTATATCATTTTTTATATATTTTATATAATGTAATAAAGAAAAACACCCCTTCTGCC 720  
Qy 761 TTTTCACTGTGTGGAGTTTCTGGAGTGAGCACTACGCCCTAAGCGGACATTCATGTG 820  
Db 721 TTTTCACTGTGTGGAGTTTCTGGAGTGAGCACTACGCCCTAAGCGGACATTCATGTG 780  
Qy 821 GGCATTTCTTGGAGCTCGCAGCTCCGGAAGTGTGAGCTTCATGACAGCATTTTGT 880  
Db 781 GGCATTTCTTGGAGCTCGCAGCTCCGGAAGTGTGAGCTTCATGACAGCATTTTGT 840  
Qy 881 GAACAGCAAGCTCAATAAATAAATAAATATTTTTCATTCATTCACCTC 987  
Db 901 AGAAGCAAGCTCAATAAATAAATAAATATTTTTCATTCATTCACCTC 947

RESULT 4

T72311  
ID T72311 standard; cDNA; 947 BP.  
AC T72311;  
DT 10-SEP-1997 (first entry)  
DE Human multiple tumour suppressor gene 1.  
KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ds.



Db 1 ATGGAGCCGGCGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGGCCGG 60  
QY 101 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGTGCGCTGCCCAACGCA 160  
Db 61 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGTGCGCTGCCCAACGCA 120  
QY 161 CCGAATAGTACGGTCGGAGCGCATCCAGGTATCATGATGGCAGCGCCGAGTGGCG 220  
Db 121 CCGAATAGTACGGTCGGAGCGCATCCAGGTATCATGATGGCAGCGCCGAGTGGCG 180  
QY 221 GAGCTGCTGCTCCACGGCGGGAGCCCACTGCGCCGACCCGCCACTCTCACCCGA 280  
Db 181 GAGCTGCTGCTCCACGGCGGGAGCCCACTGCGCCGACCCGCCACTCTCACCCGA 240  
QY 281 CCGTGCACGACGCTCCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGGGCC 340  
Db 241 CCGTGCACGACGCTCCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGGGCC 300  
QY 341 GGGCGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 400  
Db 301 GGGCGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 360  
QY 401 CTGGGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 460  
Db 361 CTGGGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 420  
QY 461 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 520  
Db 421 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 480  
QY 521 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 580  
Db 481 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 540  
QY 581 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 640  
Db 601 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 660  
QY 701 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 760  
Db 661 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 720  
QY 761 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 820  
Db 721 TTTTAAATGCTGCTGCTTTTAAAGTATAGAGCTTCCCTGAGTATAGAGCTT 780  
QY 821 GGCATTTCTTGGAGCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACAAAGCATTTGT 880  
Db 781 GGCATTTCTTGGAGCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACAAAGCATTTGT 840  
QY 881 GACTAGGAGCTCAGGGGGTACTGCTTCTTGGTACACTGCTAGCAATGTC 940  
Db 841 GACTAGGAGCTCAGGGGGTACTGCTTCTTGGTACACTGCTAGCAATGTC 900  
QY 941 AGAACCAAGCTCAAAATAAAATAAAATTTTTCATTCATTCACCTC 987  
Db 901 AGAACCAAGCTCAAAATAAAATAAAATTTTTCATTCATTCACCTC 947

RESULT 6  
V53851  
ID V53851 standard; cDNA; 947 BP.  
AC V53851;  
DT 04-DEC-1998 (first entry)  
DE Coding sequence 3 of the multiple tumour suppressor 1.  
KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;  
KW somatic mutation; gene therapy; ds.  
OS Homo sapiens.  
PN U55801236-A.

PD 01-SEP-1998. 480810.  
PF 07-JUN-1995; US-480810.  
PR 07-JUN-1995; US-480810.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215086.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PR 17-MAR-1995; WO-003316.  
PA (MVR1-) MYRIAD GENETICS INC.  
PI Kamb A;  
DR WPI: 98-494842/42.  
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
PS Claim 1: Fig 17: 73bp; English.  
CC This is the nucleotide sequence of the multiple tumour suppressor 1  
CC (MTS-1) gene, used in the method of the invention. The MTS gene  
CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
CC standard nucleic hybridisation techniques, of patient samples. The  
CC mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.  
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

Query Match 94.9%; Score 943.8; DB 1; Length 947;  
Best Local Similarity 99.8%; Pred. No. 4.1e-203;  
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 ATGGATCCGGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGCCACGGCCGG 100  
Db 1 ATGGAGCGCGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGCCACGGCCGG 60  
QY 101 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCGAGCGGTGCGCTGCCCAACGCA 160  
Db 61 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCGAGCGGTGCGCTGCCCAACGCA 120  
QY 161 CCGAATAGTACGGTCGGAGCGCATCCAGGTATCATGATGGCAGCGCCGAGTGGCG 220  
Db 121 CCGAATAGTACGGTCGGAGCGCATCCAGGTATCATGATGGCAGCGCCGAGTGGCG 180  
QY 221 GAGCTGCTGCTCCACGGCGGGAGCCCACTGCGCGGACCCGCCACTCTCACCCGA 280  
Db 181 GAGCTGCTGCTCCACGGCGGGAGCCCACTGCGCGGACCCGCCACTCTCACCCGA 240  
QY 281 CCGTGCACGACGCTCCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGGGCC 340  
Db 241 CCGTGCACGACGCTCCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGGGCC 300  
QY 341 GGGCGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 400  
Db 301 GGGCGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 360  
QY 401 CTGGGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 460  
Db 361 CTGGGCGGCTGGACGTGCGCATGCTGGGCGGCTGCTGGGCGGCTGCTGGGCGG 420  
QY 461 AACCATGCCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGGATTGAAGAACCA 520  
Db 421 AACCATGCCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGGATTGAAGAACCA 480  
QY 521 AGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTACCGAAGGTCTTACAGGGCC 580  
Db 481 AGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTACCGAAGGTCTTACAGGGCC 540  
QY 581 ACAACTGCCCCCGCCACAAACCCACCCCGGCTTTCGTAGTATAGAGCTT 640





PN WO9409135-A.  
PD 28-APR-1994.  
PF 18-OCT-1993; U09945.  
PR 16-OCT-1992; US-963308.  
PA 17-DEC-1992; US-991997.  
PI (COLD-) COLD SPRING HARBOR LAB.  
DR Beach DH, Xiong Y;  
PI WPI: 94-151320/18.  
DR P-PSDB; R53401.  
PT Detection of subunit components of cyclin complexes - used for  
PT diagnosing transformation of a cell and developing inhibitors and  
PT activators, partic for cancer treatment  
PS Claim 15; Page 39-40; 45pp; English.  
CC The cell cycle gene implicated most strongly in oncogenesis is the  
CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a  
CC locus activated by translocation to an immunoglobulin gene enhancer  
CC in some B-cell lymphomas and leukaemias. D-type cyclin, cyclin  
CC dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and  
CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many  
CC combinatorial variations of the components e.g. cyclin D1 or D3 and  
CC CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may  
CC have a subtly different role in the cell cycle or in different cell  
CC types. Cellular transformation by DNA tumour viruses such as SV40  
CC is associated with selective subunit rearrangement of the cyclin D  
CC complexes. In virally transformed cells, CDK4 totally dissociates  
CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton  
CC polypeptide (p16). This nucleotide sequence encodes a 16 kDa  
CC protein, designated p16INK4 which binds to and inhibits CDK4. This  
CC polypeptide was discovered to show many similarities to p16.  
CC Reagents, such as monoclonal antibodies, can be developed that  
CC recognise the interactions between the CDK's cyclins, PCNA and low  
CC molecular weight polypeptides and can therefore be used to identify  
CC the state of transformation of a cell.  
SQ Sequence 948 BP; 215 A; 270 C; 266 G; 197 T;

Query Match 94.3%; Score 937.6; DB 1; Length 948;  
Best Local Similarity 99.6%; Pred. No. 1e-201; Mismatches 0; Gaps 0;  
Matches 940; Conservative 0; Indels 4;

QY 51 CGCGCGGAGCAGCATGCGGCTTCTGGCTGACCTGGCTGGCGCGCGCGCGCGGCTC 110  
DB 5 CGCGCAGGCGAGCATGGAGCCCTTGGCTGACTGGCTGGCGCGCGCGCGCGGCTC 64  
QY 111 GGGTAGAGGAGTTCGGCGCGCTCTGTGAGCGGTGGCGCTGCGCCACGACGCAAGTAGTT 170  
DB 65 GGGTAGAGGAGTTCGGCGCGCTCTGTGAGCGGTGGCGCTGCGCCACGACGCAAGTAGTT 124  
QY 171 ACGGTGGAGGCGGATCCAGGTCTATGATGATGGCGCGGTGGCGCTGCGCCACGACGCAAGTAGTT 230  
DB 125 ACGGTGGAGGCGGATCCAGGTCTATGATGATGGCGCGGTGGCGCTGCGCCACGACGCAAGTAGTT 184  
QY 231 TGGTCCACGCGCGGAGCGCCCAACTGGCGCGGCGCGCGCGCTCTCACCACGCGCGCGCGCG 290  
DB 185 TGGTCCACGCGCGGAGCGCCCAACTGGCGCGGCGCGCGCGCTCTCACCACGCGCGCGCGCG 244  
QY 291 ACGGTGGCGGAGGCGGTTCTTGGACACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 350  
DB 245 ACGGTGGCGGAGGCGGTTCTTGGACACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 304  
QY 351 TGGACGTGCGCGGATGCTGTGGGCGCGCTGTCCCGTGGACCTGGCTGAGGAGCTGGGCGCATC 410  
DB 305 TGGACGTGCGCGGATGCTGTGGGCGCGCTGTCCCGTGGACCTGGCTGAGGAGCTGGGCGCATC 364  
QY 411 GCGATGTCGACGCGTACTTGGCGCGGCTGTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470  
DB 365 GCGATGTCGACGCGTACTTGGCGCGGCTGTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 424  
QY 471 GCATAGATGCGCGGAGGAGTCCCTCAGACATCCCGCGATCCCGCGATCCCGCGATCCCGCGATCCG 530  
DB 425 GCATAGATGCGCGGAGGAGTCCCTCAGACATCCCGCGATCCCGCGATCCCGCGATCCCGCGATCCG 484  
QY 531 AGAACCCTCGGGAAACTTAGATCATCATAGTCACCGAAGGTCTCTACAGGGCGCCACAACTGCC 590

DB 485 AGAACCCTCGGGAAACTTAGATCATCATAGTCACCGAAGGTCTCTACAGGGCGCCACAACTGCC 544  
QY 591 CGGCCACACACCACCCCGCTTTCGTTAGTTTTCATTTAGAAAATAGAGCTTTTAAATAATGT 650  
DB 545 CGGCCACACACCACCCCGCTTTCGTTAGTTTTCATTTAGAAAATAGAGCTTTTAAATAATGT 604  
QY 651 CTTGCCCTTTTAACGTAGATATAGCTTCCCGCACTACCGTAAATGTCATTTATATCAT 710  
DB 605 CTTGCCCTTTTAACGTAGATATAGCTTCCCGCACTACCGTAAATGTCATTTATATCAT 664  
QY 711 TTTTATATATTTCTTATAAAATGTAATAAAAGAAAACACCGCTTCTGCTTTTCACTGT 770  
DB 665 TTTTATATATTTCTTATAAAATGTAATAAAAGAAAACACCGCTTCTGCTTTTCACTGT 724  
QY 771 GTTGGAGTTTCTGGAGTGAGCACTCACGCCCTTAAGCGCACATTCATGTGGGCACTTTCTT 830  
DB 725 GTTGGAGTTTCTGGAGTGAGCACTCACGCCCTTAAGCGCACATTCATGTGGGCACTTTCTT 784  
QY 831 GCGAGCTCGCAGCCTCCGGAAGCTGTGCATTCATGACAAGCATTTTGTGAACCTAGGGA 890  
DB 785 GCGAGCTCGCAGCCTCCGGAAGCTGTGCATTCATGACAAGCATTTTGTGAACCTAGGGA 844  
QY 891 AGCTCAGGGGGTGTACTGGCTTCTCTGTGAGTCACACTGTAGCAAAATGCAGAACCAAG 950  
DB 845 AGCTCAGGGGGTGTACTGGCTTCTCTGTGAGTCACACTGTAGCAAAATGCAGAACCAAG 904  
QY 951 CTCATAATAAAATAAAATTTATTTTCACTTCACTCAAAAAA 994  
DB 905 CTCATAATAAAATAAAATTTATTTTCACTTCACTCAAAAAA 948

RESULT 9  
T00744 ID T00744 standard; cDNA: 1131 BP.  
AC T00744;  
DT 08-MAY-1996 (first entry)  
DE Multiple tumour suppressor 1 exon 1 beta (MTS1E1beta) gene ORF.  
KW Multiple tumour suppressor; MTS1E1beta; cancer; diagnosis; assay;  
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;  
KW pancreas; breast; thyroid; open reading frame; ORF; exon 1; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Cds 338..655 /\*tag= a  
FT WO9525813-Al.  
PN 28-SEP-1995.  
PF 17-MAR-1995; U03537.  
PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215087.  
PR 18-MAR-1994; US-215086.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (UTAH) UNIV UTAH RES FOUND.  
PI Cannon-Albright LA, Kamb A, Skolnick MH;  
DR WPI: 95-344626/44.  
DR P-PSDB; R81700.  
PT Detecting polymorphism associated with cancer pre:disposition - also  
PT DNA, vectors and host cells e.g. for gene or protein replacement  
PT therapy and drug screening  
PS Example 7; Pages 100-101; 148pp; English.  
CC An individual can be diagnosed as having a predisposition to cancer  
CC by detecting an alteration in the wild type multiple tumour  
CC suppressor (MTS) gene, using gene probes which hybridise to the  
CC MTS1E1beta gene ORF T00744 (which encodes R81700). The above assay  
CC can also be used in the diagnosis and prognosis of melanoma,  
CC lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.  
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 80.6%; Score 801; DB 1; Length 1131;  
Best Local Similarity 100.0%; Pred. No. 4.7e-171;





PT useful for the diagnosis of cancers related to MTS1E1-beta  
PT mutation(s) and their treatment  
PS Claim 1; Fig 12; 72pp; English.

CC This cDNA sequence encodes a human multiple tumour suppressor protein,  
CC MTS1E1-beta. The MTS gene locus is also referred to as the familial  
CC melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line  
CC mutations in MTS genes can be used in the diagnosis of predisposition to  
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,  
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,  
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum.  
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 80.6%; Score 801; DB 1; Length 1131;  
Best Local Similarity 100.0%; Pred. No. 4.7e-171;  
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CCAGGTGATGATGGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGCGGA 246  
DB 331 CCAGGTGATGATGGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGCGGA 390  
QY 247 GCCCAACTGCGCGGCGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGG 306  
DB 391 GCCCAACTGCGCGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGG 450  
QY 307 CTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 366  
DB 451 CTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 510  
QY 367 CTGGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 426  
DB 511 CTGGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 570  
QY 427 CCTGCGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 486  
DB 571 CCTGCGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 630  
QY 487 AGTCCCTAGACATCCCGGATGAAAGAACAGAGAGGCTCTGAGAAACCTCGGGAAC 546  
DB 631 AGTCCCTAGACATCCCGGATGAAAGAACAGAGAGGCTCTGAGAAACCTCGGGAAC 690  
QY 547 TTAGATCATGATCAGGAGGCTCTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 606  
DB 691 TTAGATCATGATCAGGAGGCTCTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 750  
QY 607 CGCTTTCTGAGTCTTTTATGAGAAATAGAGCTTTTAAATATGCTCTGCTTTTAAAGCTA 666  
DB 751 CGCTTTCTGAGTCTTTTATGAGAAATAGAGCTTTTAAATATGCTCTGCTTTTAAAGCTA 810  
QY 667 GATATAAGCCTTCCCGCCTACCTACCTAAATGTCCTATTTATATATTTTATATTTCTTA 726  
DB 811 GATATAAGCCTTCCCGCCTACCTACCTAAATGTCCTATTTATATATTTTATATTTCTTA 870  
QY 727 TAAATATGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 786  
DB 871 TAAATATGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 930  
QY 787 GTGAGCACTACGCGCTTAAGGCGACATTCATGTGGGATTTCTTTCGAGGCTTCGACGCT 846  
DB 931 GTGAGCACTACGCGCTTAAGGCGACATTCATGTGGGATTTCTTTCGAGGCTTCGACGCT 900  
QY 847 CCGGAAGCTGTGCACTTCATGACAAAGCATTTTGTGAAGTGGAGGCTCAGGGGGTTAC 906  
DB 991 CCGGAAGCTGTGCACTTCATGACAAAGCATTTTGTGAAGTGGAGGCTCAGGGGGTTAC 1050  
QY 907 TGGCTTCTTGTGATCAGCTAGCAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCA 966  
DB 1051 TGGCTTCTTGTGATCAGCTAGCAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCA 1110  
QY 967 ATTATTTTCATTCATTCACCT 987  
DB 1111 ATTATTTTCATTCATTCACCT 1131

RESULT 13  
V53830

ID V53830 standard; cDNA; 1131 BP.  
AC V53830;  
DE 04-DEC-1998 (first entry)  
DT Coding sequence 1 of the multiple tumour suppressor MTS1E1S.  
KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;  
KW somatic mutation; gene therapy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT 338..655  
FT CDS  
FT /tag- a  
FT /product- "human MTS1E1S"

US5801236-A.  
01-SEP-1998.  
07-JUN-1995; 480810.  
07-JUN-1995; US-480810.  
18-MAR-1994; US-214582.  
18-MAR-1994; US-215086.  
18-MAR-1994; US-215087.  
14-APR-1994; US-227369.  
01-JUN-1994; US-251938.  
17-MAR-1995; WO-003316.  
(MYRI-) MYRIAD GENETICS INC.  
PI RMB A;  
DR WPI; 98-494842/42.  
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
PS Example 7; Column 73-76; 73pp; English.

CC This is the nucleotide sequence of the multiple tumour suppressor  
CC (MTS1E1S) gene, used in the method of the invention. The MTS gene  
CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
CC standard nucleic hybridisation techniques, of patient samples. The  
CC mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.  
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 80.6%; Score 801; DB 1; Length 1131;  
Best Local Similarity 100.0%; Pred. No. 4.7e-171;  
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CCAGGTGATGATGGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGCGGA 246  
DB 331 CCAGGTGATGATGGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGCGGA 390  
QY 247 GCCCAACTGCGCGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGG 306  
DB 391 GCCCAACTGCGCGGCGGCGGCGGAGTGGCGGAGTGGTCTCTCCACGGCGG 450  
QY 307 CTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 366  
DB 451 CTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 510  
QY 367 CTGGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 426  
DB 511 CTGGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 570  
QY 427 CCTGCGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 486  
DB 571 CCTGCGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 630  
QY 487 AGTCCCTAGACATCCCGGATGAAAGAACAGAGAGGCTCTGAGAAACCTCGGGAAC 546

Db 631 AGTCTCTCAGACATCCCGATTGAAGAACACAGAGAGGCTTGAGAAACCTCGGGAAC 690  
QY 547 TTAGATCATCAGTACCGAAGTCTTACAGGGCCACAACTGCCCGGCCCAACCCACCC 606  
Db 691 TTAGATCATCAGTACCGAAGTCTTACAGGGCCACAACTGCCCGGCCCAACCCACCC 750  
QY 607 CGCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGCTGCTTTTAACGTA 666  
Db 751 CGCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGCTGCTTTTAACGTA 810  
QY 667 GATATAAGCTTCCCGACCTACCGTAAATGTCATTTATATATATATATATATATCTTA 736  
Db 811 GATATAAGCTTCCCGACCTACCGTAAATGTCATTTATATATATATATATATCTTA 870  
QY 727 TAAAAATGTAAAAAGAAAACACCGCTTCTGCTTTTCTACTGCTGTGGAGTTTCTGGA 786  
Db 871 TAAAAATGTAAAAAGAAAACACCGCTTCTGCTTTTCTACTGCTGTGGAGTTTCTGGA 930  
QY 787 GTGAGCACTCAGCCCTTAAGCGACATTCATGTGGGCAATTTCTTGGAGGCTCGCAGCCT 846  
Db 931 GTGAGCACTCAGCCCTTAAGCGACATTCATGTGGGCAATTTCTTGGAGGCTCGCAGCCT 990  
QY 847 CCGGAAGCTGTGACATTCATGACAAGCATTTTGTGAAGTGGGAGGCTCAGGGGGTTAC 906  
Db 991 CCGGAAGCTGTGACATTCATGACAAGCATTTTGTGAAGTGGGAGGCTCAGGGGGTTAC 1050  
QY 907 TGGCTTCTTGTAGTACACTGTAGCAAAATGCGAGAACAAGCTCAAAATAAAATAAA 966  
Db 1051 TGGCTTCTTGTAGTACACTGTAGCAAAATGCGAGAACAAGCTCAAAATAAAATAAA 1110  
QY 967 ATTATTTTCATTCATTCACCTC 987  
Db 1111 ATTATTTTCATTCATTCACCTC 1131

## RESULT 14

V70594  
ID V70594 standard; cDNA: 1131 BP.  
AC V70594;  
DT 03-FEB-1999 (first entry)  
DE cDNA encoding a human multiple tumour suppressor 1E1-beta protein.  
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 338..655  
FT /tag= a  
FT /product= MTS1E1-beta  
PN US5843756-A.  
PD 01-DEC-1998.  
PF 28-JUL-1995; 058735.  
PR 28-JUL-1995; US-508735.  
PR 07-JUN-1995; US-487033.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Jiang P, Kamb A, Stone S;  
DR WPI; 99-044585/04.  
DR P-PSDB; W80525.  
PT Mouse multiple tumour suppressor gene segment - useful for primer design  
PS Example 8: Fig 12A-B; 80pp; English.  
CC The present sequence encodes a human multiple tumour suppressor 1E1-beta (MTS1E1-beta) protein. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, CC thyroid, pancreas, uterus and kidneys.  
SQ Sequence 1131 BP; 231 A; 327 C; 344 G; 229 T;  
Query Match 80.6%; Score 801; DB 1; Length 1131;  
Best Local Similarity 100.0%; Pred. No. 4.7e-171;  
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 187 CCAGGTATGATGATGGCAGCGCCCGAGTGGCGGAGCTGCTGCTCCACGCGCGGA 246

Db 331 CCAGGTATGATGATGGCAGCGCCCGAGTGGCGAGCTGCTGCTCCACGCGCGGA 390  
QY 247 GCCCAACTGGCGGACCGCCGACTCTCACCGACCCGCTGCAGAGCTGCGCGGAGGG 306  
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QY 367 CTGGGGCGCTGCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCGGATGCTCCAGCGTA 426  
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QY 427 CTGCGCGGGGCTGCGGGGGGACACAGAGCAGTAACCATGCCGCATAGATGCCCGGA 486  
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QY 487 AGTCCCTCAGACATCCCGATTGAAAGAACACAGAGAGGCTCTGAGAAAGCTCGGGAAC 546  
Db 631 AGTCCCTCAGACATCCCGATTGAAAGAACACAGAGAGGCTCTGAGAAAGCTCGGGAAC 690  
QY 547 TTAGATCATCAGTCACCGAAGTCCCTACAGGGCCACAAGTGGCCGCCACCAACCC 606  
Db 691 TTAGATCATCAGTCACCGAAGTCCCTACAGGGCCACAAGTGGCCGCCACCAACCC 750  
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QY 667 GATATAAGCTTCCCGACCTACCGTAAATGTCATTTATATATATATATATATCTTA 726  
Db 811 GATATAAGCTTCCCGACCTACCGTAAATGTCATTTATATATATATATATATCTTA 870  
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QY 787 GTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGGCAATTTCTTGGAGGCTCGCAGCCT 846  
Db 931 GTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGGCAATTTCTTGGAGGCTCGCAGCCT 990  
QY 847 CCGGAAGCTGTGACATTCATGACAAGCATTTTGTGAAGTGGGAGGCTCAGGGGGTTAC 906  
Db 991 CCGGAAGCTGTGACATTCATGACAAGCATTTTGTGAAGTGGGAGGCTCAGGGGGTTAC 1050  
QY 907 TGGCTTCTTGTAGTACACTGTAGCAAAATGCGAGAACAAGCTCAAAATAAAATAAA 966  
Db 1051 TGGCTTCTTGTAGTACACTGTAGCAAAATGCGAGAACAAGCTCAAAATAAAATAAA 1110  
QY 967 ATTATTTTCATTCATTCACCTC 987  
Db 1111 ATTATTTTCATTCATTCACCTC 1131

## RESULT 15

T74051  
ID T74051 standard; cDNA: 1420 BP.  
AC T74051;  
DT 16-MAR-1998 (first entry)  
DE CDK inhibitory fusion protein coding sequence #1.  
KW Fusion gene; CDK inhibitor; cyclin-dependent kinase; p27 gene; p16 gene; chimeric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder; tissue degeneration; therapy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 4..1179  
FT /tag= a  
FT misc\_feature 4..24  
FT /tag= b  
FT /note= "poly-His tag"



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 02:16:34 ; Search time 86.37 Seconds  
(without alignments)  
1583.079 Million cell updates/sec

Title: US-09-016-869A-1  
Perfect score: 994  
Sequence: 1 CGAGAGGGGAGAGACAC.....CATTCTACTCAAAAAA 994

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
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7: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	994	100.0	994	4	US-08-627-610-1
2	994	100.0	994	4	US-08-306-511A-1
3	994	100.0	994	4	US-08-893-274-1
4	994	100.0	994	5	US-08-581-918A-1
5	994	100.0	994	6	PCT-US95-04636-1
6	943.8	94.9	947	2	US-08-474-177-36
7	943.8	94.9	947	2	US-08-487-033-36
8	943.8	94.9	947	2	US-08-480-810-36
9	943.8	94.9	947	3	US-08-508-735-36
10	943.8	94.9	947	3	US-08-848-251-36
11	943.8	94.9	947	4	US-08-486-047-36
12	943.8	94.9	947	5	US-09-120-130-36
13	943.8	94.9	947	5	US-09-115-252-36
14	937.6	94.3	948	1	US-08-154-913-3
15	937.6	94.3	948	6	PCT-US93-09945-3
16	875.2	88.0	960	5	US-08-581-918A-23
17	801	80.6	1131	1	US-08-474-177-13
18	801	80.6	1131	2	US-08-487-033-13
19	801	80.6	1131	2	US-08-480-810-13
20	801	80.6	1131	3	US-08-508-735-13
21	801	80.6	1131	4	US-08-848-251-13
22	801	80.6	1131	4	US-08-486-047-13
23	801	80.6	1131	5	US-09-120-130-13
24	801	80.6	1131	5	US-09-115-252-13
25	705.4	71.0	1420	1	US-08-589-981-1
26	467.8	47.1	471	1	US-08-474-177-1

27	467.8	47.1	471	2	US-08-487-033-1	Sequence 1, Appl
28	467.8	47.1	471	2	US-08-480-810-1	Sequence 1, Appl
29	467.8	47.1	471	3	US-08-508-735-1	Sequence 1, Appl
30	467.8	47.1	471	4	US-08-848-251-1	Sequence 1, Appl
31	467.8	47.1	471	4	US-08-486-047-1	Sequence 1, Appl
32	467.8	47.1	471	5	US-09-120-130-1	Sequence 1, Appl
33	467.8	47.1	471	5	US-09-115-252-1	Sequence 1, Appl
34	310.4	31.2	1187	1	US-08-474-177-4	Sequence 4, Appl
35	310.4	31.2	1187	2	US-08-487-033-4	Sequence 4, Appl
36	310.4	31.2	1187	2	US-08-480-810-4	Sequence 4, Appl
37	310.4	31.2	1187	3	US-08-508-735-4	Sequence 4, Appl
38	310.4	31.2	1187	4	US-08-848-251-4	Sequence 4, Appl
39	310.4	31.2	1187	4	US-08-486-047-4	Sequence 4, Appl
40	310.4	31.2	1187	5	US-09-120-130-4	Sequence 4, Appl
41	310.4	31.2	1187	5	US-09-115-252-4	Sequence 4, Appl
42	305.4	30.7	502	5	US-08-581-918A-34	Sequence 34, Appl
43	285.6	28.7	751	1	US-08-474-177-15	Sequence 15, Appl
44	285.6	28.7	751	2	US-08-487-033-15	Sequence 15, Appl
45	285.6	28.7	751	2	US-08-480-810-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-08-627-610-1  
; Sequence 1, Application US/08627610  
; Patent No. 591997  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Definho, Ronald A.  
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle  
; TITLE OF INVENTION: Regulation  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,610  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 994 base pairs  
; TYPE: nucleic acid  
; TOPOLOGY: linear  
; STRANDEDNESS: both  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 41..508  
; US-08-627-610-1

Query Match 100.0%; Score 994; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 4.9e-225;



Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGGAGCATGATCCGGCGGGGGAG 60  
DB 1 CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGGAGCATGATCCGGCGGGGGAG 60  
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DB 121 GGTGGGGCGCTGCTGGAGGGGTGGCGCTGCCAACGACCCAGCTAGTACGGTCGGAG 180  
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DB 361 CGATGCTGGGGCGCTGCTGGCGGTGGACCTGGCTGGAGAGCTGGGCCATCGCATGTCG 420  
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; Sequence 1, Application US/08306511A  
; Patent No. 5962316  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,511A  
; FILING DATE: 14-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 41..508  
; US-08-306-511A-1

Query Match 100.0%; Score 994; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 4.9e-225;  
Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGGAGCATGATCCGGCGGGGGAG 60  
DB 1 CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGGAGCATGATCCGGCGGGGGAG 60  
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Db 841 CAGCCTCGGAAGCTGTGAGTCTATGACAAAGCATTTTGTGAAGTGGAGGCTCAGGG 900
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RESULT 4
US-08-581-918A-1
; Sequence 1, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordpad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581.918A
; FILING DATE: 02-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US-08/497.214
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346.147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 41..508
; US-08-581-918A-1
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Query Match 100.0%; Score 994; DB 5; Length 994;  
Best Local Similarity 100.0%; Pred. No. 4,9e-225; Indels 0; Gaps 0;  
Matches 994; Conservative 0; Mismatches 0;

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QY 1 CGGAGAGGGGAGAAACAGACAACGGCGGGGAGGAGCAGCATGATCGGCGGGGAG 60
Db 1 CGGAGAGGGGAGAAACAGACAACGGCGGGGAGGAGCAGCATGATCGGCGGGGAG 60
QY 61 CAGCATGGAGCCTTCGGCTGACTGCTGGCCACGGCCGCGGGTGGGTAGAGGA 120
Db 61 CAGCATGGAGCCTTCGGCTGACTGCTGGCCACGGCCGCGGGTGGGTAGAGGA 120
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Db 301 GGAGGGCTTCTTGACACACGCTGTGTGCTGACCGCGGGCGGGTGGAGCTGCG 360
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Db 361 CGATGCTGGGGCGCTGCTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCATGTCG 420
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601 CAACCCCGCTTCGTAGTTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCTGCCCTTTT 660  
661 AACGTAGATATAAGCCCTCCCGCCACTACCGTAAATGCCATTATATCATTTTATATA 720  
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661 AACGTAGATATAAGCCCTCCCGCCACTACCGTAAATGCCATTATATCATTTTATATA 720  
721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCCTTTTCTACTGTGTGGAGTTT 780  
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721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCCTTTTCTACTGTGTGGAGTTT 780  
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781 TCTGGAGTGAGCACTCACGCCCTTAAGCGACATTCATGTGGGCATTTCTTCGAGGCTCG 840  
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841 CAGCCTCCGGAAGCTGCGACTTCATGACAAGCATTTTGTGAAGTGGGAAGCTCAGGGG 900  
901 GGTACTGCTCTCTTTGAGTCACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA 960  
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901 GGTACTGCTCTCTTTGAGTCACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA 960  
961 AATAAAATTTATTTTCAATTCATTCACCTCAAAAAA 994  
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RESULT 5

PCT-US95-04636-1  
; Sequence 1, Application PC/TUS9504636  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04636  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/346,147  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 994 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 41..508

PCT-US95-04636-1

Query Match 100.0%; Score 994; DB 6; Length 994;  
Best Local Similarity 100.0%; Pred. No. 4.9e-225;  
Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGAGAGGGGAGACAGACAGCGCGCGGGGAGCAGCATGGATCCGGCGCGGGAG 60  
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61 CAGCATGGAGCCTTCGGCTGACTGGCTGCCAGCGCGCGGGGCTGGGTAGAGGA 120  
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QY 121 GGTGCGGGCGCTGCTGGAGGCGGTGGCGTGCACACGACCGAAATAGTTACGGTGGAG 180  
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Db 241 CGCGGAGCCCAACTGCGCGGACCCCGCCACTCTCACCCGACCGCTGCACGACGCTGCCG 300  
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Db 301 GGAGGCGCTTCCTGGACACGCTGCTGGTGTGCACCGCGCGGGCGCGGCTGGACGTGG 360  
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Db 361 CGATGCTGGGCGCTGCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCGCGATGCTGC 420  
QY 421 ACGGTACCTGCGCGGCTGCGGGGACACGAGGCGAGTAACTACCATGCCGATAGATGC 480  
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Db 421 ACGGTACCTGCGCGGCTGCGGGGACACGAGGCGAGTAACTACCATGCCGATAGATGC 480  
QY 481 CGCGGAAGTCCCTCAGACATCCCGGATTGAAAGAACACGAGAGGCTCTGAGAACTCG 540  
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Db 481 CGCGGAAGTCCCTCAGACATCCCGGATTGAAAGAACACGAGAGGCTCTGAGAACTCG 540  
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Db 601 CCACCCCGCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCTGCCCTTT 660  
QY 661 AACGTAGATATAAGCCTTCCCGCCACTACCGTAAATGCCATTATATCATTTTATATA 720  
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Db 661 AACGTAGATATAAGCCTTCCCGCCACTACCGTAAATGCCATTATATCATTTTATATA 720  
QY 721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCCTTTTCTACTGTGTGGAGTTT 780  
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Db 721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCCTTTTCTACTGTGTGGAGTTT 780  
QY 781 TCTGGAGTGAGCACTCACGCCCTTAAGCGCACATTCATGTGGGCATTTCTTCGAGGCTCG 840  
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Db 781 TCTGGAGTGAGCACTCACGCCCTTAAGCGCACATTCATGTGGGCATTTCTTCGAGGCTCG 840  
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Db 961 AATTAATTTTTCATTCATTCATCAAAAAA 994

RESULT 6  
US-08-474-177-36  
Sequence 36, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ. ID. NO. 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 947 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 151  
OTHER INFORMATION: /note= "Splice site acceptor."  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 458  
OTHER INFORMATION: /note= "Splice site acceptor."

US-08-474-177-36

Query Match 94.9%; Score 943.8; DB 1; Length 947;  
Best Local Similarity 99.8%; Pred. No. 3e-213;  
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 41 ATGGATCCGGCGGGGAGCAGCATGGAGCCTTGGCTGACTGGCTGGCCACGCGCGCG 100  
Db 1 ATGGAGCCGGCGGGGAGCAGCATGGAGCCTTGGCTGACTGGCTGGCCACGCGCGCG 60  
QY 101 GCCCGGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGCTGGCGTCCCAAGCA 160  
Db 61 GCCCGGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGCGGGGCGCTGCCCAAGCA 120  
QY 161 CCGAATAGTTACGTCGGAGCGCCGATCCAGGTTCATGATGGCGAGCGCCGAGTGGCG 220  
Db 121 CCGAATAGTTACGTCGGAGCGCCGATCCAGGTTCATGATGGCGAGCGCCGAGTGGCG 180  
QY 221 GAGCTGCTGCTCCACGGCGGGAGCCCACTGGCGCGACCCCGCCACTCTCAACCGGA 280  
Db 181 GAGCTGCTGCTCCACGGCGGGAGCCCACTGGCGCGACCCCGCCACTCTCAACCGGA 240  
QY 281 CCGTGCACGACGCTGCCGGGAGGCTTCTTGGACACGCTGGTGGCTGCACCGGCC 340  
Db 241 CCGTGCACGACGCTGCCGGGAGGCTTCTTGGACACGCTGGTGGCTGCACCGGCC 300  
QY 341 GGGGCGGCTGGACGTGCGCGATGCTGGGGCGCTGTGCCCTGGACCTGGCTGAGGAG 400  
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QY 401 CTGGGCGATCGGATGTGCGACGGTACTGCGCGCGGCTGCGGGGGGCGCACGAGGCGAGT 460  
Db 361 CTGGGCGATCGGATGTGCGACGGTACTGCGCGCGGCTGCGGGGGGCGCACGAGGCGAGT 420  
QY 461 AACCATGCGCGCATAGATGCCGCGAAGTCCCTCAGACATCCCGATTGAAAGAACCCAG 520  
Db 421 AACCATGCGCGCATAGATGCCGCGAAGTCCCTCAGACATCCCGATTGAAAGAACCCAG 480  
QY 521 AGAGGCTCTGAGAACTCGGAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 580  
Db 481 AGAGGCTCTGAGAACTCGGAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 540  
QY 581 ACAACTGCCCGCCGACACCCCGCTTTCGTAGTTTTCATTAGAAAAATAGAGCTT 640  
Db 541 ACAACTGCCCGCCGACACCCCGCTTTCGTAGTTTTCATTAGAAAAATAGAGCTT 600  
QY 641 TTAATAATGTCCTGCTTTAAGCTAGATATAAGCTTCCCGCCTACCTACCTAAATGTCCA 700  
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QY 821 GGCATTTCTTGGAGCTCGCAGCCTCCGAGCTGTGCACTTCATGACAAGCATTTGT 880  
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Db 841 GAAGTAGGAAGCTCAGGGGGTTACTGGCTTCTTTAGTACACTGCTAGCAAAATGGC 900  
QY 941 AGAACCAAGCTCAATATAAATAAATAAATTTTTCATTTCATTCATC 987  
Db 901 AGAACCAAGCTCAATATAAATAAATAAATTTTTCATTTCATTCATC 947  
RESULT 7



NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
TELEPHONE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 947 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 151  
OTHER INFORMATION: /note= "splice site acceptor."  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 458  
OTHER INFORMATION: /note= "splice site acceptor."

US-08-480-810-36

Query Match 94.9%; Score 943.8; DB 2; Length 947;  
Best Local Similarity 99.8%; Pred. No. 3e-213;  
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 41 ATGGATCGGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGCCCGCG 100  
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Db 1 ATGGAGCGGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGCCCGCG 60  
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Qy 101 GCCCGGGTCGGGTAGAGAGAGGTGGCGGCGCTGCTGGAGCGGTGGCGCTGCCCAACGCA 160  
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Db 61 GCCCGGGTCGGGTAGAGAGAGGTGGCGGCGCTGCTGGAGCGGGGCGCTGCCCAACGCA 120  
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Qy 161 CCGAATAGTTACGGTCGGAGGCCGATCCAGTCATGATGATGGCAGCGCCGAGTGGCG 220  
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Qy 221 GAGCTGCTGTCTCCACGGCGGGAGGCCAACTGCGCCGACCCCGCACTCTCACCCGA 280  
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Db 181 GAGCTGCTGTCTCCACGGCGGGAGGCCAACTGCGCCGACCCCGCACTCTCACCCGA 240  
|||||

Qy 281 CCCGTGCACGACGCTCCCGGGAGGCTTCTGACACGCTGGTGGTGCACCGGGCC 340  
|||||

Db 241 CCCGTGCACGACGCTCCCGGGAGGCTTCTGACACGCTGGTGGTGCACCGGGCC 300  
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Qy 341 GGGCGGGGCTGGACGTCGCGATGCTGGGGCGCTGTCGCCGTGGACCTGGCTGAGGAG 400  
|||||

Db 301 GGGCGGGGCTGGACGTCGCGATGCTGGGGCGCTGTCGCCGTGGACCTGGCTGAGGAG 360  
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Qy 401 CTGGGCCATCGCGATGTCGACGGTACTGCGCGCGGCTGCGGGGGGACAGAGGAGT 460  
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Db 361 CTGGGCCATCGCGATGTCGACGGTACTGCGCGCGGCTGCGGGGGGACAGAGGAGT 420  
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Qy 461 AACCATGCCCGCATAGATGCCGCGAAGTCCCTCAGACATCCCGGATGAAAGAACGAG 520  
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Db 421 AACCATGCCCGCATAGATGCCGCGAAGTCCCTCAGACATCCCGGATGAAAGAACGAG 480  
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Qy 521 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGATCACCAGAGTCTTACAGGGCC 580  
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Db 481 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGATCACCAGAGTCTTACAGGGCC 540  
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Qy 581 ACAACTGCCCGCGCCACCAACCCCGCTTTCGTAGTTTTCATTTAGAAAAATAGAGCTT 640  
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Db 541 ACAACTGCCCGCGCCACCAACCCCGCTTTCGTAGTTTTCATTTAGAAAAATAGAGCTT 600  
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|||||

Db 601 TTAATAATGCTTCCCTTTTAACTAGATATAAGCCCTTCCCGCTACCGTAAATGTCCA 660  
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Qy 701 TTTATATCATTTTTTATATATTTTATAAATAATGTAATAAAGAAAAACACCGCTTCTGCC 760  
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Db 661 TTTATATCATTTTTTATATATTTTATAAATAATGTAATAAAGAAAAACACCGCTTCTGCC 720  
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Qy 761 TTTTCACTGTTGGAGTTTCTGGAGTGAGCACTACGCGCTAAGCGCACATTCATGTG 820  
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Db 721 TTTTCACTGTTGGAGTTTCTGGAGTGAGCACTACGCGCTAAGCGCACATTCATGTG 780  
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Qy 821 GGCATTTCTTCGGAGCTCGCAGCTCCGGAAGCTGTCGACTTCATGACAGCAATTTGT 880  
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Qy 881 GAACTAGGGAAGCTCAGGGGGTTTACTGGCTTCTTTGAGTCACACTGCTAGCAAAATGGC 940  
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Db 841 GAACTAGGGAAGCTCAGGGGGTTTACTGGCTTCTTTGAGTCACACTGCTAGCAAAATGGC 900  
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Qy 941 AGAACCAAGCTCAATAAATAAATAATTTTTCATTCATTCATCTACTC 987  
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RESULT 9

US-08-508-735-36  
; Sequence 36, Application US/08508735  
; Patent No. 5843756

GENERAL INFORMATION:  
; APPLICANT: Stone, Steven  
; APPLICANT: Jiang, Ping  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000









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1  FILING DATE: 01-JUN-1994
2  PRIOR APPLICATION DATA:
3  APPLICATION NUMBER: US 08/215,087
4  FILING DATE: 18-MAR-1994
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: US 08/215,086
7  FILING DATE: 18-MAR-1994
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 08/227,369
10 FILING DATE: 14-APR-1994
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/214,582
13 FILING DATE: 18-MAR-1994
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Ihnen, Jeffrey L.
16 REGISTRATION NUMBER: 26,957
17 REFERENCE/DOCKET NUMBER: 24884-109348-B
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 202-962-4810
20 TELEFAX: 202-962-8300
21 INFORMATION FOR SEQ ID NO: 36:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 947 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: double
26 TOPOLOGY: linear
27 MOLECULE TYPE: cDNA
28 HYPOTHETICAL: NO
29 ANTI-SENSE: NO
30 ORIGINAL SOURCE:
31 ORGANISM: Homo sapiens
32 FEATURE:
33 NAME/KEY: misc_feature
34 LOCATION: 151
35 OTHER INFORMATION: /note= "Splice site"
36 FEATURE:
37 NAME/KEY: misc_feature
38 LOCATION: 458
39 OTHER INFORMATION: /note= "Splice site"
40 US-08-486-047-16

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Query Match	94.9%	Score 943.8	DB 4	Length 947
Best Local Similarity	99.8%	Pred. No. 3e-213		
Matches 945	Conservative 0	Mismatches 2	Indels 0	Gaps 0
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Db	61	GCCCGGGTCCGGTAGAGAGAGTGGCGCGTGTCTGAGGGGGGCGCTGCCCAACGCA	120	
Qy	161	CCGAATAGTAGGTCGGAGGCCGATCAGGTCATGATGTTGGGAGCGCCCGAGTGGG	220	
Db				
Db	121	CCGAATAGTAGGTCGGAGGCCGATCAGGTCATGATGTTGGGAGCGCCCGAGTGGG	180	
Qy	221	GAGCTGCTGCTCTCCACGGCGGAGGCCCAACTGCGCGACCCCGCCACTCTCACCCGA	280	
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Db	181	GAGCTGCTGCTCTCCACGGCGGAGGCCCAACTGCGCGACCCCGCCACTCTCACCCGA	240	
Qy	281	CCCGTGACAGAGTGTCCCGGAGGGCTTCCTGGACAGCTGGTGGTGTGACCGGGCC	340	
Db				
Db	241	CCCGTGACAGAGTGTCCCGGAGGGCTTCCTGGACAGAGCTGGTGGTGTGACCGGGCC	300	
Qy	341	GGGCGGGCTGGAGTGGCGGATCCCTGGGGCCGCTCTGCCGTGGACCTGGCTGAGGAG	400	
Db				
Db	301	GGGCGGGCTGGAGTGGCGGATCCCTGGGGCCGCTCTGCCGTGGACCTGGCTGAGGAG	360	
Qy	401	CTGGGCCATCGATGTGCGACAGGTACCTGCGCGCGGCTGCGGGGGGACACGAGGCGAGT	460	
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RESULT 12  
US-09-120-130-36  
; Sequence 36, Application US/09120130  
; Patent No. 6037462  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS1 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,130  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,810  
; FILING DATE:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,810  
; FILING DATE:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086

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; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: /note= "splice site acceptor."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 458
; OTHER INFORMATION: /note= "splice site acceptor."
;
; US-09-120-130-36

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Best Local Similarity 99.8%; Pred. No. 3e-213;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 ATGATCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCGACGCGCGCG 100
DB 1 ATGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCGACGCGCGCG 60

QY 101 GCCCGGGTCCGGTAGAGGAGTCCGGCGCGCTGCTGGAGCGGTGGCGCTGCCCAACGCA 160
DB 61 GCCCGGGTCCGGTAGAGGAGTCCGGCGCGCTGCTGGAGCGGTGGCGCTGCCCAACGCA 120

QY 161 CCGAATAGTTACGGTCGGAGCGCATCCAGTGCATGATGATGGCGACGCCCGCGAGTGGCG 220
DB 121 CCGAATAGTTACGGTCGGAGCGCATCCAGTGCATGATGATGGCGACGCCCGCGAGTGGCG 180

QY 221 GAGTGTCTGTCTCCACGCGGGGAGCCCAACTGCGCGACCCCGGCACTCTCACCCGA 280
DB 181 GAGTGTCTGTCTCCACGCGGGGAGCCCAACTGCGCGACCCCGGCACTCTCACCCGA 240

QY 281 CCGTGACACGCGTCCCGGGAGGGCTTCCTGGACACGCTGGTGTGCTGCACCGGGCC 340
DB 241 CCGTGACACGCGTCCCGGGAGGGCTTCCTGGACACGCTGGTGTGCTGCACCGGGCC 300

QY 341 GGGCGCGGTGACAGTGCAGTGCCTGGGCGGTGCTGCCGTGGACCTGGCTGAGGAG 400
DB 301 GGGCGCGGTGACAGTGCAGTGCCTGGGCGGTGCTGCCGTGGACCTGGCTGAGGAG 360

QY 401 CTGGCCATCGCATGTCGACGCGTACCTGCGCGCGCTGCGGGGGCCACGAGGCGAGT 460
DB 361 CTGGCCATCGCATGTCGACGCGTACCTGCGCGCGCTGCGGGGGCCACGAGGCGAGT 420

QY 461 AACCATGCCCGCATAGATGCCGGGAGGTCCTCTAGACATCCCGGATTCGAAAGAACCG 520
DB 421 AACCATGCCCGCATAGATGCCGGGAGGTCCTCTAGACATCCCGGATTCGAAAGAACCG 480

QY 521 AGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCATGTCACCGAGGTCCTACAGGGCC 580

; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: /note= "splice site acceptor."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 458
; OTHER INFORMATION: /note= "splice site acceptor."
;
; US-09-120-130-36

RESULT 13
US-09-115-252-36
; Sequence 36, Application US/09115252
; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,252
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
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;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 948 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: CDNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 19..465  
;; US-08-154-915-3

Query Match 94.3%; Score 937.6; DB 1; Length 948;  
Best Local Similarity 99.6%; Pred. No. 8.6e-212;  
Matches 940; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 51 CGGCGGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGCGGGGTC 110  
DB 5 CGGCACGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGCGGGGTC 64  
QY 111 GGTAGAGAGGTGGCGCGCTGCTGGAGCGGTGGCGCTGCCAAACGACCCGAATAGTT 170  
DB 65 GGTAGAGAGGTGGCGCGCTGCTGGAGCGGTGGCGCTGCCAAACGACCCGAATAGTT 124  
QY 171 ACGTCTGGAGCGGCATCCAGGTCAATGATGGCAGCGCCGCGAGTGGCGAGCTGCTGC 230  
DB 125 ACGTCTGGAGCGGCATCCAGGTCAATGATGGCAGCGCCGCGAGTGGCGAGCTGCTGC 184  
QY 231 TGTCTCACGCGCGGAGCCCAACTGGCCGACCGCCGCACTCTCACCCGACCGTGGACG 290  
DB 185 TGTCTCACGCGCGGAGCCCAACTGGCCGACCGCCGCACTCTCACCCGACCGTGGACG 244  
QY 291 ACGTCTGGCGGAGGGCTTCCTGGACACGCTGGTGGTGTGCTGACCGCGCGGGCGGGC 350  
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QY 351 TGGACGTGCGCGATGCTGGGGCGCTGCGCCGTGGACCTGGCTGGAGAGTGGGCCATC 410  
DB 305 TGGACGTGCGCGATGCTGGGGCGCTGCGCCGTGGACCTGGCTGGAGAGTGGGCCATC 364  
QY 411 GCGATGTGCGACGCTACCTGCGCGCGGTGCGGGGGGACCCAGAGGAGTAACCATGCCC 470  
DB 365 GCGATGTGCGACGCTACCTGCGCGCGGTGCGGGGGGACCCAGAGGAGTAACCATGCCC 424  
QY 471 GCATAGATGCGCGGAGGTCCCTCAGACATCCCGGATGTAAGAAACAGAGAGGCTCTG 530  
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QY 531 AGAAACCTCGGGAACCTTAGATCATCATCAGTACGACGAGTCTACAGGCGCAACTGCCC 590  
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QY 591 CCGCACAAACCAACCCGCTTCGTAGTTTCATTTAGAAAAATAGAGCTTTTAAAAATGT 650  
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QY 651 CCTGCCCTTTAACCTAGATATAAGCTTCCCGCACTACCGTAAATGTCATTTATATCAT 710  
DB 605 CCTGCCCTTTAACCTAGATATAAGCTTCCCGCACTACCGTAAATGTCATTTATATCAT 664  
QY 711 TTTTATATATCTTATAAAATGTAAAAAGAAACACCGCTTCTGCGCTTTTCACGTGT 770  
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QY 831 GCGAGCCTCGCAGCCTCGGGAAGCTGTGAGCTTCATGACAGCAATTTGTGAACCTAGGGA 890  
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QY 891 AGCTCAGGGGGTTACTGGCTTCTCTTGAGTCACACTGTAGCAATGGCAGAACCAAG 950  
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; APPLICANT:  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related  
; TITLE OF INVENTION: Thereto  
; NUMBER OF SEQUENCES: 4  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
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; APPLICATION NUMBER: PCT/US93/09945  
; FILING DATE:  
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; FILING DATE: 16-OCT-1992  
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; FILING DATE: 17-DEC-1992  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 948 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 19..465  
; PCT-US93-09945-3

Query Match 94.3%; Score 937.6; DB 6; Length 948;  
Best Local Similarity 99.6%; Pred. No. 8.6e-212;  
Matches 940; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 51 CGGCGGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGGGGTC 110  
DB 5 CGGCACGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGGGGTC 64  
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QY 411 GCGATGTGCGACGCTACCTGCGCGCGGTGCGGGGGGACCCAGAGGAGTAACCATGCCC 470

Db 365 GCGATGTCGCACGGTACTCGCGCGGCTGCGGGGGCACCAGAGGCAGTAACCATGCC 424  
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Qy 951 CTCAAATAAAATAAAATTTTTCATTTCACTCAAAAAA 994  
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Mon Jul 24 10:14:12 2000

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: July 21, 2000, 00:08:05 ; Search time 1049.06 Seconds  
(without alignments)  
4178.378 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: em\_est2.\*
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- 103: gb\_gss7.\*
- 104: gb\_gss8.\*
- 105: gb\_gss9.\*
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- 108: em\_gss7.\*
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- 110: em\_gss9.\*
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- 112: em\_gss11.\*
- 113: gb\_gss10.\*
- 114: gb\_gss11.\*
- 115: em\_gss12.\*
- 116: gb\_gss12.\*



117: gb\_gss13:\*  
118: gb\_gss14:\*  
119: gb\_gss15:\*  
120: gb\_gss16:\*  
121: gb\_gss17:\*  
122: gb\_gss18:\*  
123: gb\_gss19:\*  
124: em\_gss13:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	652.4	65.6	689	38	AI337358 tb98f09.x
C 2	625.2	62.9	679	38	AI379336 tc73903.x
C 3	560	56.3	568	79	AW664294 hi09c04.x
C 4	558.6	56.2	566	39	AI394605 tq13q05.x
C 5	558.2	56.2	590	45	AI871381 wi18111.x
C 6	546.4	55.0	579	45	AI870879 wl77d11.x
C 7	545.8	54.9	604	45	AI859822 wm20h06.x
C 8	544.2	54.7	580	38	AI362049 qy39f07.x
C 9	543.8	54.7	579	36	AI198233 q155d12.x
C 10	535	53.8	729	44	AI817709 wk25c11.x
C 11	530	53.3	563	46	AI954684 wq34h12.x
C 12	526	52.9	774	44	AI765096 w148h08.x
C 13	525.2	52.8	531	42	AI633790 tt28e10.x
C 14	523.2	52.6	528	45	AI885362 w192h04.x
C 15	522.8	52.6	528	42	AI638416 tt31q03.x
C 16	521.2	52.6	708	38	AI363262 qy56f03.x
C 17	521.2	52.4	579	62	AW06218 w293q05.x
C 18	519	52.2	648	71	AW328496 ds02h12.x
C 19	518.6	52.2	599	28	AA557137 n174h05.s
C 20	484.8	48.8	531	44	AI806771 wf15a09.x
C 21	483	48.6	505	36	AI186333 qd30a08.x
C 22	482.8	48.6	496	71	AW328497 ds02h12.y
C 23	464.2	46.7	494	69	AW190459 xl15e01.x
C 24	463	46.6	533	32	AA877595 nr07f06.s
C 25	460.4	46.3	531	33	AA946585 oq49e06.s
C 26	460.2	46.3	474	70	AW246625 2821897.3
C 27	451.2	45.4	563	44	AI869175 w150c04.x
C 28	427	43.0	465	44	AI818660 wk89c11.x
C 29	426.8	42.9	450	35	AI091727 ow59f04.x
C 30	422.8	42.5	426	45	AI859893 wm23a09.x
C 31	416.2	41.9	421	40	AI479957 tm73d10.x
C 32	407.4	41.0	419	46	AI937552 w78f11.x
C 33	406.6	40.9	454	21	AA098836 zn44e11.s
C 34	405.4	40.8	419	41	AI500223 tm94b03.x
C 35	403.6	40.6	417	39	AI454154 ut-r-BT0-
C 36	403.2	40.6	447	36	AI149429 gc72f05.x
C 37	399.2	40.2	441	20	AA055664 z175f06.s
C 38	398.8	40.1	532	20	AA069792 zn15a11.s
C 39	391	39.3	401	44	AI803069 tj47a12.x
C 40	380.6	38.3	398	34	AI040505 ox14f08.s
C 41	377.2	37.9	548	32	AA903110 ox52b03.s
C 42	371.8	37.4	410	21	AA076328 zn18a12.s
C 43	365.8	36.8	369	38	AI363480 qy69f05.x
C 44	364.8	36.7	395	36	AI199084 q140a06.x
C 45	362.8	36.5	374	28	AA579918 nm88a08.s

ALIGNMENTS

RESULT 1  
LOCUS AI337358/6  
DEFINITION tb98f09.x1 NCI\_CGAP\_Col6 Homo sapiens cDNA clone IMAGE:2062409 3' similar to SW:CDN2\_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR

A ; mRNA sequence.  
AI337358  
VERSION AI337358.1 GI:4074285  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 689)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036732.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html  
Insert length: 1023 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 469.  
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/clone="IMAGE:2062409"  
/clone\_lib="NCI\_CGAP\_Col6"  
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/lab\_host="DH10B"  
/note="Organ: colon; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site: 1; Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1057416-106255, and 1144584-1145351)."  
BASE COUNT 162 a 170 c 186 g 167 t 4 others  
ORIGIN  
Query Match 65.8%; Score 652.4; DB 38; Length 689;  
Best Local Similarity 98.4%; Pred. No. 6.8e-149;  
Matches 678; Conservative 0; Mismatches 9; Indels 2; Gaps 2;  
Qy 296 GCCCGGAGGCTTCCTGGACACGCTGGTGTCTGCACCGCGCGCGGCGCTGCAC 355  
Db 689 GCCCGGAGGCTTCCTGGACACCGCTGGTGTCTGCACCGCGCGCGGCGCTGCAC 630  
Qy 356 GTGCGCATGCTGGGCGCGCTCTGCCGTGGACCTGTGCTGAGGAGCTGGGCCATCGCGAT 415  
Db 629 GTGCGCATGCTGGGCGCGCTCTGCCGTGGACCTGTGCTGAGGAGCTGGGCCATCGCGAT 570  
Qy 416 GTGCGAC-GGTACTGCGCGCGGCTGGCGGGGGCCAGAGGAGTAAACCATGCCCGCAT 474  
Db 569 GTGCGACGGGTACTGCGCGCGGCTGGCGGGGGCCAGAGGAGTAAACCATGCCCGCAT 510  
Qy 475 AGATGCCGCGGAGGCTCCCTCAGACATCCCGGATTGAAGAACCAGAGAGGCTCTGAGAA 534  
Db 509 AGATGCCGCGGAGGCTCCCTCAGACATCCCGGATTGAAGAACCAGAGAGGCTCTGAGAA 450  
Qy 535 ACCTCGGGAACCTTAGATCATCATGCTACCGGAAGTCTCTACAGGGGCCACAA-CTGCCCCCG 593  
Db 449 ACCTCGGGAACCTTAGATCATCATGCTACCGGAAGTCTCTACAGGGGCCACAACTGCCCCCG 390

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QY 594 CCACACCCACCCGCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCT 653
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QY 654 GCCTTTTAAAGGTAGATATAAGCCTTCCCGCACTACCGTAATGTCCTTATATATATATTT 713
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Db 329 GCCTTTTAAAGGTAGATATAAGCCTTCCCGCACTACCGTAATGTCCTTATATATATTT 270
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QY 714 TTATATATTTTAAATAATGTAATAAGAAACACCGCTTCGCTTTTCACTGTGTT 773
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Db 269 TTATATATTTTAAATAATGTAATAAGAAACACCGCTTCGCTTTTCACTGTGTT 210
|||||
QY 774 GGAGTTTCTGGAGTAGAGCACTCACGCCCTAAGCGCACATTCATGCGCATTTCTTGGC 833
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Db 209 GGAGTTTCTGGAGTAGAGCACTCACGCCCTAAGCGCACATTCATGCGCATTTCTTGGC 150
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QY 834 AGCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACAAAGCATTTTGTGAAGTACGGAAGC 893
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Db 149 AGCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACAAAGCATTTTGTGAAGTACGGAAGC 90
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QY 894 TCAGGGGGTACTGGCTTCTTGTAGTCACACTGTAGCAAAATGGCAGAACCAAGCTC 953
|||||
Db 89 TCAGGGGGTACTGGCTTCTTGTAGTCACACTGTAGCAAAATGGCAGAACCAAGCTC 30
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QY 954 AATAAAATAAATAATTTTCAATTCATT 982
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Db 29 AATAAAATAAATAATTTTCAATTCATT 1
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RESULT 2
AI379336/c
LOCUS
DEFINITION
tc73g03.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070292
3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA
FORM ;, mRNA sequence.

ACCESSION
AI379336
VERSION
AI379336.1 GI:4189189
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 679)
AUTHORS
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
On Dec 5, 1997 this sequence version replaced gi:2662837.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2070292"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NHM, pregnant uterus
NHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
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consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 158 a 154 c 178 g 182 t 7 others
ORIGIN

Query Match 62.9%; Score 625.2; DB 38; Length 679;
Best Local Similarity 97.0%; Pred. No. 2.9e-142;
Matches 644; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

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Db 673 GCACCGCGCGCGCGGCTGGACGTGCGCATGCGTGGGGCGGCTGCGCGTGGACCT 615
|||||
QY 391 GGTGAGGAGCTGGGCGCATGCGCATGCGCATGCGTGGGGCGGCTGCGGGGGGCGAC 450
|||||
Db 614 GCTGAAGGAGCTGGGCAATCGCATGTCGACGCTACCTGCGCGCGGCTGCGGGGGGCGAC 555
|||||
QY 451 CAGAGGCGAGTAACCATGCGCGCATAGATGCGCGGGAAGTCCCTCAGACATCCCGATTG 510
|||||
Db 554 CAGAGGCGAGTANCCATGCGCGCATAGATGCGCGGGAAGTCCCTCAGACATCCCGATTG 495
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QY 511 AAAGAACACAGAGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCATGACGGAAGGTC 570
|||||
Db 494 AAAGAACACAGAGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCATGACGGAAGGTC 435
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QY 571 CTACAGGGCCACAACTGCCCCGCCACACCCACCGCGCTTCGTAGTTTTCATTTAGAA 630
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Db 434 CTACAGGGCCACAACTGCCCCGCCACACCCACCGCGCTTCGTAGTTTTCATTTAGAA 375
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QY 631 AATGAGCTTTTAAAAATGCTCTGCTTTTAAAGTAGATATAAGCTTCCCCCCTACCG 690
|||||
Db 374 AATGAGCTTTTAAAAATGCTCTGCTTTTAAAGTAGATATAAGCTTCCCCCCTACCG 315
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Db 314 TAAATGTCATTTATATATCATTTTATATATCTTATAAAATGTAATAAAAGAAAAACAC 255
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|||||
Db 254 CGCTTCTGCTTTTCACTGTTGGAGTTTCTGGAGTAGAGCACTCACGCCCTTAAGCGCA 195
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QY 811 CATCATGTTGGGATTTCTTGGCAGGCTCGCAGCTCCGGAAGCTGTCGACTTCATGACA 870
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Db 194 CATTCATGTTGGGATTTCTTGGCAGGCTCGCAGCTCCGGAAGCTGTCGACTTCATGACA 135
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QY 931 AGCAATGTCGAGAACCAAGCTCAAAATAAAATATAAAATTTTTCATTCATTCCTCAAA 990
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QY 991 AAAA 994
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Db 14 AAAA 11

RESULT 3
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LOCUS
DEFINITION
AW664294 568 bp mRNA EST 06-APR-2000
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION
AW664294
VERSION
AW664294.1 GI:7456835
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 568)
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AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Jul 7, 1999 this sequence version replaced gi:5407043.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life  
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[image.llnl.gov/image/hml/iresources.shtml](http://image.llnl.gov/image/hml/iresources.shtml)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 417.  
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/lab\_host="DH10B"  
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;  
Site 1: SalI; Site 2: NotI; Cloned unidirectionally.  
Primer: Oligo dT. Library constructed by Life  
Technologies."  
BASE COUNT 144 a 118 c 149 g 157 t  
ORIGIN  
Query Match 56.3%; Score 560; DB 79; Length 568;  
Best Local Similarity 99.1%; Pred. No. 2.2e-126;  
Matches 563; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 416 GTCGACGGTACCTCGCGGGCTCGCGGGGCGCCAGGAGGAGTAACTGCGCGCAT 475  
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Qy 476 GATGCGCGGAGGTCCTCAGACATCCCGATTGAAGAGACAGAGGCTCTGAGAAA 535  
Db 508 GATGCGCGGAGGTCCTCAGACATCCCGATTGAAGAGACAGAGGCTCTGAGAAA 449  
Qy 536 CTTGGGAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCCACAACTGCCCGGCC 595  
Db 448 CTTGGGAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCCACAACTGCCCGGCC 389  
Qy 596 ACAACCCACCGCTTCGTAGTTTTCATTAGAAAATAGAGCTTTTAAAAATGTCCTGC 655  
Db 388 ACAACCCACCGCTTCGTAGTTTTCATTAGAAAATAGAGCTTTTAAAAATGTCCTGC 329  
Qy 656 CTTTAAAGCTAGATATAGCCTTCCCGACCTACCGTAATGTCATTTATATATTTT 715  
Db 328 CTTTAAAGCTAGATATAGCCTTCCCGACCTACCGTAATGTCATTTATATATTTT 269  
Qy 716 ATATATTTCTTAAAAATGTAAAAAGAAAACACCGCTTCTGCTTTTCACTGTGTTGG 775  
Db 268 ATATATTTCTTAAAAATGTAAAAAGAAAACACCGCTTCTGCTTTTCACTGTGTTGG 209  
Qy 776 AGTTTCTGGAGTAGAGACTACAGCCCTCAAGGCGACATTCATGTGGGCAATTTCTTGCAG 835  
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Qy 836 CTTGCGACCTCCGAGCTGTCGACTTCATCAGAACATTTTGTGAAGTGGGAGCTC 895  
Db 148 CTTGCGACCTCCGAGCTGTCGACTTCATCAGAACATTTTGTGAAGTGGGAGCTC 89  
Qy 896 AGGGGGTGTACTGGCTTCTCTTGTAGTCACTGCTAGCAATGGCAGAACCAAAAGCTCAA 955  
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Db 88 AGGGGGTACTGCTTCTTGTAGTCACACTGCTAGCAATGGCAGAACCAAAAGCTCAA 29  
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Db 28 ATAAAAATAAAATATTTTCATTCATTC 1  
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DEFINITION tg13q05.x1 NCI-CGAP-CLL1 Homo sapiens cDNA clone IMAGE:2108696 3',  
similar to SW:CDN2.HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR  
A: contains LTR9.B3 TAR1 repetitive element; mRNA sequence.  
AI394605  
ACCESSION AI394605.1 GI:4224152  
VERSION AI394605.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 566)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
M.D., Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 755 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 457.  
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/lab\_host="DH10B"  
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TGTTACCAATCTGAAGTGGAGCGCGCATTCGTTTTTTTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 113 a 159 c 175 g 118 t 1 others  
ORIGIN  
Query Match 56.2%; Score 558.6; DB 39; Length 566;  
Best Local Similarity 99.1%; Pred. No. 4.8e-126;  
Matches 561; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 170 TACGTCGAGGCGCATCCAGGTCATGATGGCGCGCCGAGTGGCGAGCTGCTG 229  
Db 566 TACGTCGAGGCGCATCCAGGTCATGATGGCGCGCGAGTGGCGAGCTGCTG 507  
Qy 230 CTGCTCCAGCGCGGAGCCCACTGGCGGACCCCGGCACTCTCACCAGCCGTCGAC 289  
Db 506 CTGCTCCAGCGCGGAGCCCACTGGCGGAGCCCACTCTCACCAGCCGTCGAC 447  
Qy 290 GACGCTGCCGGGAGGGCTTCTCTGGACACGCTGTGTGTGCTGCACCGCGGCGCGG 349

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Db 446 GACGTCGCCGGAGGGCTTCTGACACGCTGGTGGTCTGACACGGCGCGCGCGG 387
QY 350 CTGGAGCTGCGGATGCTCCCTGGGGCGCTCTGCCCTGGACCTGGCTGAGGAGCTGGGCCAT 409
Db 386 CTGGAGCTGCGGATGCTCCCTGGGGCGCTCTGCCCTGGACCTGGCTGAGGAGCTGGGCCAT 327
QY 410 CCGGATGTCGCACGCTACCTGCGCGGGTGGGGGGGACACAGAGGAGTAAACATGCC 469
Db 326 CCGGATGTCGCACGCTACCTGCGCGGGTGGGGGGGACACAGAGGAGTAAACATGCC 267
QY 470 CCGATAGATGCCCGGAGGTCCTCAGACATCCCGGATTGAAAGAACAGAGAGGCTCT 529
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QY 530 GAGAACTCCGGGAACTTAGATCATCATGACACCGGAGGTCCTACAGGCGCCACAACTGCC 589
Db 206 GAGAACTCCGGGAACTTAGATCATCATGACACCGGAGGTCCTACAGGCGCCACAACTGCC 147
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Db 146 CCGGCGACACCCACCCCGCTTCTGAGTTTTCATTTAGAAAATAGAGCTTTAAAAATG 87
QY 650 TCCTGCTTTTAAAGTAGATATAAGCTTCCCGGCTACCGTAAATGTCATTTATATCA 709
Db 86 TCCTGCTTTTAAAGTAGATATAAGCTTCCCGGCTACCGTAAATGTCATTTATATCA 27
QY 710 TTTTATATATTTCTTAAAAATGT 735
Db 26 TTTTATATATTTCTTAAAAATGT 1

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; mRNA sequence.
ACCESSION AI871381
VERSION AI871381.1 GI:5545430
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 845 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
Location/Qualifiers
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FEATURES
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 114 a 158 c 179 g 139 t
ORIGIN

Query Match 56.2%; Score 558.2; DB 45; Length 590;
Best Local Similarity 99.5%; Pred. No. 6e-126;
Matches 560; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 187 CCAGGTGATGATGGGAGCGCCGAGTGGCGAGCTGCTGCTCCAGCGGCGGA 246
Db 567 CCAGGTGATGATGATGGGAGCGCCGAGTGGCGAGCTGCTGCTCCAGCGGCGGA 508
QY 247 GCCCAACTGCGCGACCGCCGACCTCTCACCAGCCCGTGCACGAGCTGCCGGAGG 306
Db 507 GCCCAACTGCGCGACCGCCGACCTCTCACCAGCCCGTGCACGAGCTGCCGGAGG 448
QY 307 CTTCTGGACAGCTGGTGTGCTGCACCGCGCGCGCTGGAGCTGCGGATGC 366
Db 447 CTTCTGGACAGCTGGTGTGCTGCACCGCGCGCGCTGGAGCTGCGGATGC 388
QY 367 CTGGGCGCTCTGCCCTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGTCGACGGTA 426
Db 387 CTGGGCGCTCTGCCCTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGTCGACGGTA 328
QY 427 CTTGCGCGGCTGCGGGGCGACAGAGGCTGAGGAGTAAACATGCCCATAGATGCCGCGGA 486
Db 327 CTTGCGCGGCTGCGGGGCGACAGAGGCTGAGGAGTAAACATGCCCATAGATGCCGCGGA 268
QY 487 AGTCCCTCAGACATCCCGGATTGAAAGAACAGAGAGGCTCTGAGAAACCTCGGGAAC 546
Db 267 AGTCCCTCAGACATCCCGGATTGAAAGAACAGAGAGGCTCTGAGAAACCTCGGGAAC 208
QY 547 TTAGATCATCATCAGGAGTCTTACAGGCGCACAACTGCCCGCGCACAAACCCACC 606
Db 207 TTAGATCATCATCAGGAGTCTTACAGGCGCACAACTGCCCGCGCACAAACCCACC 148
QY 607 CGCTTTCGTAGTTTCATTTAGAAAATAGAGCTTTAAAAATGCTGCTGCTTTTACGTA 666
Db 147 CGCTTTCGTAGTTTCATTTAGAAAATAGAGCTTTAAAAATGCTGCTGCTTTTACGTA 88
QY 667 GATATAGCTTTCCCGGCTACCGTAAATGTCATTTATATATATATATATATCTTA 726
Db 87 GATATAGCTTTCCCGGCTACCGTAAATGTCATTTATATATATATATATATCTTA 28
QY 727 TAAAAATGTAAGAAAAAGAAAAACA 749
Db 27 TAAAAATGTAAGAAAAAGAAAAACA 5

RESULT 6
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LOCUS w177d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430933 3'
DEFINITION similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION AI870879
VERSION AI870879.1 GI:5544847
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 579)  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index Unpublished (1998)  
JOURNAL On May 18, 1998 this sequence version replaced gi:3136859.  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaudo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 819 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 474.

FEATURES  
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/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCAATCTCAAGTGGAGCGCGCATAGTCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaudo."  
BASE COUNT 113 a 157 c 182 g 127 t

Query Match 55.08; Score 546.4; DB 45; Length 579;  
Best Local Similarity 98.94; Pred. No. 4.5e-123;  
Matches 550; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 187 CCAGGTGATGATGGCAGCGCCGAGTGGCGGAGTGTGCTGTCTCCACGGCGCGGA 246  
DB 556 CCAGGTGATGATGGCAGCGCCGAGTGGCGGAGTGTGCTGTCTCCACGGCGCGGA 497

QY 247 GCCCAACTGCGCGACCCCGCCACTCTCACCCGACCGGTGACACGCTGCGCGGAGGG 306  
DB 496 GCCCAACTGCGCGACCCCGCCACTCTCACCCGACCGGTGACACGCTGCGCGGAGGG 437

QY 307 CTTCTTGACACGCTGTGTGCTGCACCGGCGCGGCGGTGACGTCGCGCATGC 366  
DB 436 CTTCTTGACACGCTGTGTGCTGCACCGGCGCGGCGGTGACGTCGCGCATGC 377

QY 367 CTGGGGCGCTGCGCGTGGACCTGGGTGAGGAGTGGGCCATCGCATGTCGACCGGTA 426  
DB 376 CTGGGGCGCTGCGCGTGGACCTGGGTGAGGAGTGGGCCATCGCATGTCGACCGGTA 317

QY 427 CCTCGCGCGGCTGCGGGGGGACACAGAGGAGTAACCATGCCCGCATAGATGCCGCGGA 486  
DB 316 CCTCGCGCGGCTGCGGGGGGACACAGAGGAGTAACCATGCCCGCATAGATGCCGCGGA 257

QY 487 AGGTCCCTCAGACATCCCGGATTGAAGAACACAGAGGCTCTCAGAAACCTCGGGAAC 546  
DB 256 AGGTCCCTCAGACATCCCGGATTGAAGAACACAGAGGCTCTCAGAAACCTCGGGAAC 197

QY 547 TTAGATCATAGTCACCGAAGGTCTTACAGGGGCCACAACCTGCCCGCCGACCAACCC 606  
|||||

Db 196 TTAGATCATAGTCACCGAAGGTCTTACAGGGGCCACAACCTGCCCGCCGACCAACCC 137

QY 607 CGCTTTGCTAGTTTTTCATTTAGAAAATAGAGCTTTTAAATAATGCTCTGCTTTAAAGTA 666  
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Db 136 CGCTTTGCTAGTTTTTCATTTAGAAAATAGAGCTTTTAAATAATGCTCTGCTTTAAAGTA 77

QY 567 GATATAAGCTTCCCTCCACTACCGTAATGTCATTTATATATATATATATATATCTTA 726  
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Db 76 GATATATGCTTCCCTCCACTACCGTAATGTCATTTATATATATATATATATATCTTA 17

QY 727 TAAAAATGTAAAAAG 742  
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Db 16 TAAAAATGTAAAAAG 1

RESULT 7  
LOCUS AI859822/c  
DEFINITION AI859822 604 bp mRNA EST 07-MAR-2000  
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
// mRNA sequence.

ACCESSION AI859822  
VERSION AI859822.1 GI:5513427  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 604)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)  
JOURNAL On Oct 30, 1998 this sequence version replaced gi:3811883.  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
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Seq primer: -400P from Gibco  
High quality sequence stop: 418.

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/clone\_lib="NCI-CGAP-Ut4"  
/tissue\_type="serous papillary carcinoma, high grade, 2 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #:  
11542-016"

BASE COUNT 151 a 130 c 154 g 166 t 3 others

ORIGIN

Query Match 54.9%; Score 545.8; DB 45; Length 604;  
Best Local Similarity 94.7%; Pred. No. 6.3e-123;  
Matches 574; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

QY 386 GACCTGGCTGAGAGCTGGGCCATCGCATGTCGACGGTACCTGCGCGGCTGCGGGG 445  
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Db 604 GACCTGGCTGAGAGCTGGGCCATCGCATGTCGACGGTACCTGCGCGGCTGCGGGG 545  
|||||







CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo, Ph.D.									
CDNA Library Arrayed by: Greg Lennon, Ph.D.									
DNA Sequencing by: Washington University Genome Sequencing Center									
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/brp/image/image.html									
Insert length: 613 Std Error: 0.00									
Seq primer: -400P from Gibco									
High quality sequence stop: 460.									
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/clone="IMAGE:2473223"									
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/tissue_type="pooled germ cell tumors"									
/lab_host="DH10B"									
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bernaldo."									
BASE COUNT 112 a 158 c 169 g 124 t									
ORIGIN									
Query Match 53.3%; Score 530; DB 46; Length 563;									
Best Local Similarity 98.9%; Pred. No. 4.4e-113;									
Matches 544; Conservative 0; Mismatches 5; Indels 1; Gaps 1;									
Qy	190	GTCATGATGATGGGAGCGCGGAGTGGCGGAGTGTGCTGCTCCACGGCGGAGGC	249						
Db	549	GTCATGATGATGGGAGCGCGGAGTGGCGGAGTGTGCTGCTCCACGGCGGAGGC	490						
Qy	250	CAACTGCGCGACCCCGCCACTCTCACCCGACCGTGCACGAGCTGCCCGGAGGCTT	309						
Db	489	CAACTG-GCGACCCCGCCACTCTCACCCGACCGTGCACGAGCTGCCCGGAGGCTT	431						
Qy	310	CTTGGACACGCTGGTGGTGTGTCACCGCGCGGCGCGGCTGGACGTGCGCATGCCTG	369						
Db	430	CTTGGACACGCTGGTGGTGTGTCACCGCGCGGCGCGGCTGGACGTGCGCATGCCTG	371						
Qy	370	GGGCGCTCTCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGCGACGTACCT	429						
Db	370	GGGCGCTCTCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGCGACGTACCT	311						
Qy	430	GGCGGGCTGCGGGGGGACAGAGCGAGTACCATGCCCATAGATGCCCGGAGG	489						
Db	310	GGCGGGCTGCGGGGGGACAGAGCGAGTACCATGCCCATAGATGCCCGGAGG	251						
Qy	490	TCCTCAGACATCCCGGATTGAAGAACACAGAGAGCTCTGAGAACCTCGGGAACCTTA	549						
Db	250	TCCTCAGACATCCCGGATTGAAGAACACAGAGAGCTCTGAGAACCTCGGGAACCTTA	191						
Qy	550	GATCATCAGTCACCGAGGTCCTACAGGGGCGACAACTGCCCGCGCACACCCCGCG	609						
Db	190	GATCATCAGTCACCGAGGTCCTACAGGGGCGACAACTGCCCGCGCACACCCCGCG	131						
Qy	610	TTTCGTAGTTTTCATTTAGAAATAGAGCTTTTAAATATGCTCCTGCTTTTACGTAGT	669						
Db	130	TTTCGTAGTTTTCATTTAGAAATAGAGCTTTTAAATATGCTCCTGCTTTTACGTAGT	71						
Qy	670	ATAAGCCTTCCCGCAGTACCGTAAATGTCATTTATATATATATATATATATATATAA	729						
Db	70	ATAAGCCTTCCCGCAGTACCGTAAATGTCATTTATATATATATATATATATATATAA	11						
Qy	730	AAATGTAAAA 739							

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Db 10 AAATGTAATA 1
RESULT 12
AI765096/c
LOCUS
DEFINITION
w148D08.x1 NCI_CGAP.Col6 Homo sapiens cDNA clone IMAGE:2393463 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
LTR9.b3 MER22 repetitive element ;, mRNA sequence.
ACCESSION
AI765096
VERSION
AI765096.1 GI:5231605
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -400P from Gibco
High quality sequence stop: 400.
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/tissue_type="Colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP.Col0 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaudo."
BASE COUNT 153 a 220 c 221 g 179 t 1 others
ORIGIN
Query Match 52.9%; Score 526; DB 44; Length 774;
Best Local Similarity 86.0%; Pred. No. 4.4e-118;
Matches 583; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
Qy 72 CTTCCGGCTGACTGGTGGCCACGGCCGGGGTGGGTGAGAGGAGTGGGGCGC 131
Db 706 CATCCCGGGTTCAGGGGGAGGTGGCAGGCCAGGCCAGGGCGGCCCTGTGGCCATC 647
Qy 132 TGCTGGAGCGGTGGCTGCCACGACCGACCAAGTAGTACGGTCGGAGCGGCATCCAGG 191
Db 646 GTGCTTATGCTATTGAGGAGCCACCGTTTAGGGCAGCAGCGCGTCTCTAGAACACGAG 587
Qy 192 TCATGATGATGGCAGCGCCCGAGTGGGGAGTCTGCTGCTCCACGCGCGGAGGCCA 251
Db 586 TCATGATGATGGCAGCGCCCGAGTGGGGAGTCTGCTGCTCCACGCGCGGAGGCCA 527

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/db_xref="taxon:9606"
/clone="IMAGE:2242122"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743)." Subtraction by
Bento Soares and M. Fatima Bonaldo.
BASE COUNT 107 a 144 c 163 g 116 t 1 others
ORIGIN

Query Match 52.8%; Score 525.2; DB 42; Length 531;
Best Local Similarity 99.2%; Pred. NO. 6.5e-118;
Matches 527; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 212 CGAGTGGCGAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCACT 271
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Db 531 CGAGTGGCGAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCACT 472
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QY 272 CTCACCGGACCCGTGCACGACGTGCGCGGAGGGCTTCCTGGACACGCTGTGGTGCTG 331
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|
|
Db 471 CTCACCGGACCCGTGCACGACGTGCGCGGAGGGCTTCCTGGACACGCTGTGGTGCTG 412
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|
|
QY 332 CACCGGGCGGGCGGGCTGGACGTGCGCGATGCTTGGGGCGCTGCGCCGTGGACCTG 391
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|
|
Db 411 CACCGGGCGGGCGGGCTGGACGTGCGCGATGCTTGGGGCGCTGCGCCGTGGACCTG 352
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|
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QY 392 GCTGAGGAGCTGGGCCATCGCATGTCGACGCTGCGCGGCTGCGGGGGGACCC 451
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|
|
Db 351 GCTGAGGAGCTGGGCCATCGCATGTCGACGCTGCGCGGCTGCGGGGGGACCC 292
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|
|
QY 452 AGAGGAGTAAACCATGCCGCATAGATGCGCGGAGAGTCCCTCAGACATPCCCGATTGA 511
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|
|
Db 291 AGAGGAGTAAACCATGCCGCATAGATGCGCGGAGAGTCCCTCAGACATPCCCGATTGA 232
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|
|
QY 512 AAGAACCAGAGAGCTGTGAGAACCTCGGGAACCTAGATCATCATCAGTACCGAAGTCC 571
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|
|
Db 231 AAGAACCAGAGAGCTGTGAGAACCTCGGGAACCTAGATCATCATCAGTACCGAAGTCC 172
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|
|
QY 572 TACAGGGCCAAACTGCCCCCGCCACACCCACCGCTTTCGTAGTTTTCATTAGAAA 631
|
|
|
Db 171 TACAGGGCTACACTGCCCCCGCCACACCCACCGCTTTCGTAGTTTTCATTAGAAA 112
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|
|
QY 632 ATAGAGCTTTTAAATAATGCTCCTGCTTTTAAAGCTAGATATAAGCTTCCCGCACTACCGT 691
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|
|
Db 111 ATAGAGCTTTTAAATAATGCTCCTGCTTTTAAAGCTAGATATAAGCTTCCCGCACTACCGT 52
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|
|
QY 692 AATGTCCATTTATATATATTTTATATATCTTATATAAATGTAATAAAG 742
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Db 51 AATGTCCATTTATATATATTTTATATATCTTATATAAATGTAATAAAG 1

RESULT 14
AI885362/c
LOCUS AI885362 528 bp mRNA EST 07-MAR-2000
DEFINITION w192h04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432407 3'
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A : mRNA sequence.
ACCESSION AI885362
VERSION AI885362.1 GI:5590526
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
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```
AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbrrp/image/image.html
Insert Length: 626 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGACGGCGGAGGTTTGTGTGTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 165 g 114 t
ORIGIN

Query Match 52.6%; Score 523.2; DB 45; Length 528;
Best Local Similarity 99.4%; Pred. NO. 2e-117; 3; Indels 0; Gaps 0;
Matches 525; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 215 GTGGCGGAGTGTGCTGTCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCACTCTC 274
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Db 528 GTGGCGGAGTGTGCTGTCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCACTCTC 469
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QY 275 ACCCGACCGTGCACAGCGTGCCTGGGAGGGCTTCTGGACACGCTGTGTGTGTGCAC 334
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Db 468 ACCCGACCGTGCACAGCGTGCCTGGGAGGGCTTCTGGACACGCTGTGTGTGTGCAC 409
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QY 335 CGGGCGGGCGGGCTGGACGTGCGCGATGCTTGGGGCGCTGCTGGACCTGGCT 394
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Db 408 CGGGCGGGCGGGCTGGACGTGCGCGATGCTTGGGGCGCTGCTGGACCTGGCT 349
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QY 395 GAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCGCTGCGGGGGGACCCAGA 454
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|
|
Db 348 GAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCGCTGCGGGGGGACCCAGA 289
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|
|
QY 455 GGCACTAACCATGCCCGCATAGATGCCGGGAGAGTCCCTCAGACATATCCCGATTGAAG 514
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|
|
Db 288 GGCACTAACCATGCCCGCATAGATGCCGGGAGAGTCCCTCAGACATATCCCGATTGAAG 229
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|
|
QY 515 AACCAGAGGGCTCTGAGAAACCTCGGAAACTTAGATCATCATCAGTACCGAAGTCTTAC 574
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|
|
Db 228 AACCAGAGGGCTCTGAGAAACCTCGGAAACTTAGATCATCATCAGTACCGAAGTCTTAC 169
|
|
|
QY 575 AGGGCCACAACTGCCCGCCGACCAACCCCGCTTTCGTAGTTTTCATTAGAAAAATA 634
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Db 168 AGGGCCACAACTGCCCGCCGACCAACCCCGCTTTCGTAGTTTTCATTAGAAAAATA 109
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151 ProSerAspIleProAsp 156  
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451 CCTCAGACATCCCGAT 468

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seq\_documentation\_block: 471 bp DNA PAT 29-SEP-1999  
LOCUS AR037494  
DEFINITION Sequence 1 from patent US 5801236.  
ACCESSION AR037494  
VERSION AR037494.1 GI:5955350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Kamb,A.  
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes  
JOURNAL Patent: US 5801236-A 1 01-SEP-1998;  
FEATURES  
Location/Qualifiers  
source  
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BASE COUNT 68 a 153 c 186 g 64 t  
ORIGIN

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Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
US-09-016-869A-2 x AR037494 ..

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17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34  
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51 CACGCCCGCGCCGGTGGGTAGAGAGGTGCGGGCGTGTGGAGG 100  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
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101 CGGGGGCGCTGCCAACGACCGAATAGTTACGGTCGGAGCGCGATCCAG 150  
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
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151 GTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGG 200  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
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201 CGCGAGCCCAACTCGCGGACCCCGCCACTCTCACCGACCGGTGCAG 250  
84 sPAAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
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251 ACCTGTCGGGGAGGGCTTCCTGGACACCGCTGGTGGTGTGTCACCGGGCC 300  
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
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301 GGGCGCGCTGGAGCTGGCGATGCCCTGGGGCGCTGCCCCGTGGACCT 350  
117 uAlaGluLeuLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134  
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351 GGCTGAGAGCTGGCCATCGCGATGTGCACGCTACCTGGCGCGGGTG 400  
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
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401 CGGGGGCACCAGAGCGATACCATGCCCGCATAGATGCCGCGGAAGGT 450  
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451 CCTCAGACATCCCGAT 468  
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seq\_documentation\_block: 471 bp DNA PAT 29-SEP-1999  
LOCUS AR062774  
DEFINITION Sequence 1 from patent US 5843756.  
ACCESSION AR062774  
VERSION AR062774.1 GI:5990465  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Stone,S., Jiang,P. and Kamb,A.  
TITLE Mouse MTS1 gene  
JOURNAL Patent: US 5843756-A 1 01-DEC-1998;  
FEATURES  
Location/Qualifiers  
source  
1..471  
BASE COUNT 68 a 153 c 186 g 64 t  
ORIGIN

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
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Align seg 1/1 to: AR062774 from: 1 to: 471

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17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34  
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51 CACGCCCGCGCCGGTGGGTAGAGAGGTGCGGGCGTGTGGAGG 100  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
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101 CGGGGGCGCTGCCAACGACCGAATAGTTACGGTCGGAGCGCGATCCAG 150  
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
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151 GTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGG 200  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
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201 CGCGAGCCCAACTCGCGGACCCCGCCACTCTCACCGACCGGTGCAG 250  
84 sPAAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
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251 ACCTGTCGGGGAGGGCTTCCTGGACACCGCTGGTGGTGTGTCACCGGGCC 300  
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
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301 GGGCGCGCTGGAGCTGGCGATGCCCTGGGGCGCTGCCCCGTGGACCT 350  
117 uAlaGluLeuLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134  
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
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451 CCTCAGACATCCCGAT 468

seq\_name: gb\_pat:I41148

seq\_documentation\_block: 471 bp DNA PAT 13-MAY-1997  
LOCUS I41148  
DEFINITION Sequence 1 from patent US 5624819.  
ACCESSION I41148  
VERSION I41148.1 GI:2081738  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.  
TITLE Germline mutations in the MTS gene  
JOURNAL Patent: US 5624819-A 1 29-APR-1997;  
FEATURES  
source 1..471  
Location/Qualifiers  
BASE COUNT 68 a 153 c 186 g 64 t  
ORIGIN

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
US-09-016-869A-2 x I41148 ..

Align seg 1/1 to: I41148 from: 1 to: 471

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTirLeuAl 17  
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1 ATGGAGCCGGCGGGGAGGAGCAGATGAGCCTTCGGCTGACTGGCTGGC 50  
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34  
|||||  
51 CACGGCCGGCGGGGTCGGGTAGAGAGGTGCGGGCGTGTGGAGG 100  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
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101 CGGGGGCGCTGCCCAACGCCAGATAGTTACGGTCGGAGGCCGATCCAG 150  
51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
|||||  
151 GTCATGATGATGGGAGCGCCGAGTGGGGAGCTGCTGCTCCACGG 200  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
|||||  
201 CGCGAGGCCCAACTGCGCGACCCGCCACTCTACCGACCCGTCGACG 250  
84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
|||||  
251 ACCTGCCCCGGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGG 300  
101 GlyAlaArgLeuAspValArgAspAlaTirpGlyArgLeuProValAspLe 117  
|||||  
301 GGGGGCGGCTGGAGTGGCCGATGCTGGGGCCGCTGCTGCCCTGGACCT 350  
117 uAlaGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134  
|||||  
351 GGCTGAGGAGCTGGGCATCGCGATGTCACGGTACCTGCGCGGGCTG 400  
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
|||||  
401 CGGGGGGACACAGAGGAGCAGTACCATGCCCGCATAGATGCCGGAAGT 450  
151 ProSerAspIleProAsp 156  
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451 CCTCAGACATCCCGAT 468

seq\_name: gb\_pat:AR001346

seq\_documentation\_block:  
LOCUS AR001346 947 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 36 from patent US 5739027.  
ACCESSION AR001346  
VERSION AR001346.1 GI:3963413  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Kamb,A.  
TITLE MTS1E1.beta. gene  
JOURNAL Patent: US 5739027-A 36 14-APR-1998;  
FEATURES  
source 1..947  
Location/Qualifiers  
BASE COUNT 207 a 271 c 274 g 195 t  
ORIGIN

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
US-09-016-869A-2 x AR001346 ..

Align seg 1/1 to: AR001346 from: 1 to: 947

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|||||  
1 ATGGAGCCGGCGGGGAGGAGCAGATGAGCCTTCGGCTGACTGGCTGGC 50  
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34  
|||||  
51 CACGGCCGGCGGGGTCGGGTAGAGAGGTGCGGGCGTGTGGAGG 100  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
|||||  
101 CGGGGGCGCTGCCCAACGCCAGATAGTTACGGTCGGAGGCCGATCCAG 150  
51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
|||||  
151 GTCATGATGATGGGAGCGCCGAGTGGGGAGCTGCTGCTCCACGG 200  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
|||||  
201 CGCGAGGCCCAACTGCGCGACCCGCCACTCTACCGACCCGTCGACG 250  
84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
|||||  
251 ACCTGCCCCGGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGG 300  
101 GlyAlaArgLeuAspValArgAspAlaTirpGlyArgLeuProValAspLe 117  
|||||  
301 GGGGGCGGCTGGAGTGGCCGATGCTGGGGCCGCTGCTGCCCTGGACCT 350  
117 uAlaGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134  
|||||  
351 GGCTGAGGAGCTGGGCATCGCGATGTCACGGTACCTGCGCGGGCTG 400  
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
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401 CGGGGGGACACAGAGGAGCAGTACCATGCCCGCATAGATGCCGGAAGT 450  
151 ProSerAspIleProAsp 156  
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451 CCTCAGACATCCCGAT 468



seq\_name: gb\_pat:AR037526

seq\_documentation\_block: 947 bp DNA PAT 29-SEP-1999  
LOCUS AR037526  
DEFINITION Sequence 36 from patent US 5801236.  
ACCESSION AR037526  
VERSION AR037526.1 GI:5955382  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Kamb,A.  
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes  
JOURNAL Patent: US 5801236-A 36 01-SEP-1998;  
FEATURES Location/Qualifiers  
source 1..947  
BASE COUNT 207 a 271 c 274 g 195 t  
ORIGIN

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x AR037526 ..

Align seg 1/1 to: AR037526 from: 1 to: 947

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1 ATGGAGCGCGCGCGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCG 50
||||:|||||
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
||||:|||||
51 CACGGCGCGCGCGGGGTGGGTAGAGAGGTGGGGCGCTGCTGGAGG 100
||||:|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
||||:|||||
101 CGGGGGCGCTGCCACGCCACCGAATAGTTACGGTCGGAGCGCATCCAG 150
||||:|||||
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
||||:|||||
151 GTCATGATGATGGGACGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200
||||:|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
||||:|||||
201 CGGGAGCCCAACTGCGCGACCCCGCCACTCTCACCCGACCCGTGCACG 250
||||:|||||
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
||||:|||||
251 ACGCTGCCGGGAGGGCTTCCTGGACACGCTGGTGTGCTGCACCGGGCC 300
||||:|||||
101 GlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValaspLe 117
||||:|||||
301 GGGGCGGGCTGGACGTGGCGATGCTGGGGCGGTCTGCCCGTGGACCT 350
||||:|||||
117 uAlaGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134
||||:|||||
351 GGCTGAGGAGCTGGGCCATCGCGATGTCGCACCGGTACCTCGCGCGGCTG 400
||||:|||||
134 laGlyGlyThrArgGlySerAsnHisAlaAlaArgIleAspAlaGluGly 150
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401 CGGGGGCCACGAGGCGAGTAACCATGCCCGCATAGATGCCCGGAAGGT 450
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151 ProSerAspIleProAsp 156
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451 CCTCAGACATCCCCGAT 468
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seq\_name: gb\_pat:AR062806

seq\_documentation\_block:

LOCUS AR062806 947 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 36 from patent US 5843756.  
ACCESSION AR062806  
VERSION AR062806.1 GI:5990497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Stone,S., Jiang,P. and Kamb,A.  
TITLE Mouse MTS1 gene  
JOURNAL Patent: US 5843756-A 36 01-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..947  
BASE COUNT 207 a 271 c 274 g 195 t  
ORIGIN

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x AR062806 ..

Align seg 1/1 to: AR062806 from: 1 to: 947

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||||:|||||
1 ATGGAGCGCGCGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCG 50
||||:|||||
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
||||:|||||
51 CACGGCGCGCGCGGGGTGGGTAGAGAGGTGGGGCGCTGCTGGAGG 100
||||:|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
||||:|||||
101 CGGGGGCGCTGCCACGCCACCGAATAGTTACGGTCGGAGCGCATCCAG 150
||||:|||||
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
||||:|||||
151 GTCATGATGATGGGACGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200
||||:|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
||||:|||||
201 CGGGAGCCCAACTGCGCGACCCCGCCACTCTCACCCGACCCGTGCACG 250
||||:|||||
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
||||:|||||
251 ACGCTGCCGGGAGGGCTTCCTGGACACGCTGGTGTGCTGCACCGGGCC 300
||||:|||||
101 GlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValaspLe 117
||||:|||||
301 GGGGCGGGCTGGACGTGGCGATGCTGGGGCGGTCTGCCCGTGGACCT 350
||||:|||||
117 uAlaGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134
||||:|||||
351 GGCTGAGGAGCTGGGCCATCGCGATGTCGCACCGGTACCTCGCGCGGCTG 400
||||:|||||
134 laGlyGlyThrArgGlySerAsnHisAlaAlaArgIleAspAlaGluGly 150
||||:|||||
401 CGGGGGCCACGAGGCGAGTAACCATGCCCGCATAGATGCCCGGAAGGT 450
||||:|||||
151 ProSerAspIleProAsp 156
||||:|||||
451 CCTCAGACATCCCCGAT 468
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seq\_name: gb\_pat:I41180

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seq_documentation_block:
LOCUS      I41180      947 bp      DNA      PAT      13-MAY-1997
DEFINITION Sequence 36 from patent US 5624819.
ACCESSION  I41180
VERSION    I41180.1 GI:2081770
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 947)
AUTHORS   Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE     Germ-line mutations in the MTS gene
JOURNAL   Patent: US 5624819-A 36 29-APR-1997;
FEATURES   Location/Qualifiers
            source
            1..947
            /organism="unknown"
BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN

alignment_scores:
  Quality: 789.00      Length: 156
  Ratio: 5.090        Gaps: 0
  Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:
US-09-016-869A-2 x I41180 ..
Align seg 1/1 to: I41180 from: 1 to: 947
1 MetAspProAlaAlaGlySerMetGluProSerAlaAspTrpLeuAl 17
||||:|||||
1 ATGGAGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50
17 aThrAlaAlaArgGlyArgValGluValAlaArgAlaLeuGluA 34
|||||
51 CACGGCGCGCGCGGGTGGGTAGAGAGGTGCGGCGCTGCTGGAG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|||||
101 CGGGGGCGCTGCCACGCCACCGCAATAGTTACGGTCGGAGCGGATCCAG 150
51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisG1 67
|||||
151 GTCATGATGATGGCGACGCCGCGAGTGGCGAGCTGCTGCTCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis 84
|||||
201 CGGGAGCCCACTCGCGCCACCCGCCACTCTCACCCGACCCGTCGACG 250
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
251 ACGTGCGCGGAGGGCTTCTGACACGCTGTTGTGTGTCACCGCGCC 300
101 GlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValAspLe 117
|||||
301 GGGCGCGCTGGACGTGCGCGATGCTGGGGCGCTGCTGCGCGTGACCT 350
117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
|||||
351 GGTGAGGAGCTGGCCATCGCATGTGCGACGCTGCTGCGCGCGCTG 400
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
|||||
401 CGGGGGCACCAGAGGAGTAACCATGCCGCATAGATGCCGCGGAAGGT 450
151 ProSerAspIleProAsp 156
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451 CCCTCAGACATCCCCGAT 468
seq_name: gb_pr2:HUMINK4X
seq_documentation_block:
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17 aThAlaAlaAaArgGlyArgValGluGluValuValArgAlaLeuLeuGluA 34  
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34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
|||||  
141 CGGGGGCGCTGCCCAACGACCGATAGTACGGTCGGAGCGCGATCCAG 190  
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
|||||  
191 GTCATGATGATGGCGCGCGCGAGTGGCGAGCTGCTGCTCCACGG 240  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
|||||  
241 CGCGAGCGCCAACTCGCGCGACCGCGCCACTCTCACCGACCGGTGCACG 290  
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
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291 ACGTGCCTCGCGGAGGGCTTCCTGGACACGCTGGTGTCTGCACCGGGCC 340  
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
|||||  
341 GGGCGCGCTGGACGTGCGGATGCTGGGGCGCTCTGCCCGTGGACCT 390  
117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134  
|||||  
391 GCTGAGGAGCTGGCCATTCGCGATGTCGACGGTACCTGGCGCGGCTG 440  
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
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441 CGGGGGCACCAGAGCGATACCATGCCGATAGATGCCGCGGAAGGT 490  
151 ProSerAspIleProAsp 156  
|||||  
491 CCTCAGACATCCCGAT 508

seq\_name: gb\_pat:167718

seq\_documentation\_block: 1420 bp DNA PAT 30-DEC-1997  
LOCUS I67718  
DEFINITION Sequence 1 from patent US 5672508.  
ACCESSION I67718  
VERSION I67718.1 GI:2731253  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1420)  
AUTHORS Gyuris,J., Lamphere,L. and Beach,D.  
TITLE Inhibitors of cell-cycle progression, and uses related thereto  
JOURNAL Patent: US 5672508-A 1 30-SEP-1997;  
FEATURES  
source  
1. .1420  
BASE COUNT 322 a 410 c 458 g 230 t  
ORIGIN

alignment\_scores:  
Quality: 785.00 Length: 156  
Ratio: 5.065 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
US-09-016-869A-2 x I67718 ..

Align seg 1/1 to: I67718 from: 1 to: 1420

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17 aThAlaAlaAaArgGlyArgValGluGluValuValArgAlaLeuLeuGluA 34

759 CACGCCCGCGCGCGGGTTCGGGTAGAGAGAGTGGCGCGTGTCTGGAGG 808  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
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809 CGGTGGCGCTGCCCAACGACCGATAGTACGGTCGGAGCGCGATCCAG 858  
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
|||||  
859 GTCATGATGATGGCGCGCGCGAGTGGCGAGCTGCTGCTCCACGG 908  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
|||||  
909 CGCGAGCGCCAACTCGCGCGACCGCGCCACTCTCACCGACCGGTGCACG 958  
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
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959 ACGTGCCTCGCGGAGGGCTTCCTGGACACGCTGGTGTCTGCACCGGGCC 1008  
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
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1009 GGGCGCGCTGGACGTGCGGATGCTGGGGCGCTCTGCCCGTGGACCT 1058  
117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134  
|||||  
1059 GCTGAGGAGCTGGCCATTCGCGATGTCGACGGTACCTGGCGCGGCTG 1108  
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
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1109 CGGGGGCACCAGAGCGATACCATGCCGATAGATGCCGCGGAAGGT 1158  
151 ProSerAspIleProAsp 156  
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1159 CCTCAGACATCCCGAT 1176  
seq\_name: gb\_pr4:AF115544  
seq\_documentation\_block: 793 bp mRNA PRI 01-FEB-1999  
LOCUS AF115544  
DEFINITION Homo sapiens cyclin-dependent kinase inhibitor p12 (p16INK4a) mRNA,  
alternatively spliced form, complete cds.  
ACCESSION AF115544  
VERSION AF115544.1 GI:4206166  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS Robertson,K.D. and Jones,P.A.  
TITLE Tissue-specific alternative splicing in the human INK4a/ARF cell  
cycle regulatory locus  
JOURNAL Oncogene (1998) In press  
REFERENCE 2 (bases 1 to 793)  
AUTHORS Robertson,K.D. and Jones,P.A.  
TITLE Direct Submission  
JOURNAL Submitted (21-DEC-1998) Cancer Center, University of Southern  
California, 1441 Eastlake Ave. MS 73, Los Angeles, CA 90033, USA  
FEATURES  
Location/Qualifiers  
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/map="p"  
/tissue\_type="pancreas"  
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1..351  
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/note="alternatively spliced form of p16INK4a"  
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/product="cyclin-dependent kinase inhibitor p12"  
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/db\_xref="GI:4206167"  
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BASE COUNT 153 a 213 c 300 g 127 t  
ORIGIN

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Quality: 716.50 Length: 248  
Ratio: 4.623 Gaps: 2  
Percent Similarity: 62.500 Percent Identity: 61.694  
alignment\_block:  
US-09-016-869A-2 x AF115544 ..  
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1 ATGGAGCGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50  
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34  
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51 CACGCGCGCGCGCGGGGTCTGGGTAGAGGAGTGCGGCGCTGCTGGAGG 100  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIle.G1 50  
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101 CGGGGGCGCTGCCACGCCACCGCAATAGTTACGGTCGGAGCGCATCCAG 150  
50 n..... 50  
151 GTGGGTAGAAGGCTTCGACGGGAGCAGGGGATGGCGGCGACTCTCGAG 200  
50 ..... 50  
201 GACGAAGTTTCAGCGGAATGGAAATCAGGTAGCGCTTCGATTCCTCGGA 250  
50 ..... 50  
251 AAAAGGGGAGGCTCTCTGGGAGTTTTCAGAAGGGTTTGTATATACACAGA 300  
50 ..... 50  
301 CCTCTCTCTGGCAGCGCCCTGGGGGCTTGGGAACCAAGGAGGAATG 350  
50 ..... 50  
351 AGGAGCCACCGCGGTACAGATCTCTCGAATGCTGAGAAGATCTGAAGGG 400  
51 .....ValMetMetMetGlySerAlaArgVa 59  
401 GGAACATATTGTATTAGATGGAAGTCATGATGCGCAGCGCCCTGT 450  
59 laAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProA 76  
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451 GCGGGAGCTGCTGCTCTCACCGCGCGGAGCCCACTGGCGCCGACCCCG 500  
76 laThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAsp 92  
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501 CCACCTCTACCCGACCGCTGCACAGCAGCTGCCCGGAGGGCTTCTCGAC 550  
93 ThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAl 109  
|||||||||||||||||||||||||||||||||||||||||  
551 ACGCTGGTGTGCTGCACCGCGCGGGCGCGGCTGGACGTGCGCATGC 600  
109 aTrpGlyArgLeuProValAspLeuAlaGluLeuGlyHisArgAspV 126  
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601 CTGGGGCGCTGTCGCGTGGACCTGGCTGGAGAGCTGGGCCATCGCGATG 650  
126 alAlaArgTyrLeuArgAlaAlaGlyThrArgGlySerAsnHis 142  
|||||||||||||||||||||||||||||||||||||||||  
651 TGCACGGTACCTCGCGCGGCTCGGGGGGCGCACAGAGGCGAGTAACCAT 700

143 AlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156  
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701 GCCCGCATAGATCCCGGAAGTCTCCTCAGACATCCCGCAT 742  
seq\_name: gb\_pr2:HSU26727  
seq\_documentation\_block:  
LOCUS HSU26727 1017 bp mRNA PRI 30-NOV-1995  
DEFINITION Human p16INK4/MTS1 mRNA, complete cds.  
ACCESSION U26727  
VERSION U26727.1 GI:862412  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 1017)  
AUTHORS Duro,D., Bernard,O., Della Valle,V., Berger,R. and Larsen,C.J.  
TITLE A new type of p16INK4/MTS1 gene transcript expressed in B-cell malignancies  
JOURNAL Oncogene 11 (1), 21-29 (1995)  
MEDLINE 95349933  
REFERENCE 2 (bases 1 to 1017)  
AUTHORS Larsen,C.-J.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAY-1995) Christian-Jacques Larsen, Institut de  
Genetique moleculaire, U-301 Inserm, 27, rue Juliette Dodu, Paris  
75010, France  
FEATURES  
Location/Qualifiers  
Source 1..1017  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="13 RPMI 8226"  
/chromosome="9"  
/map="9p21"  
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1..220  
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/note="Also called exon 0.18, substituted by alternative  
splicing to p16INK4 exon 1"  
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1..1017  
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/note="a frameshift between exon 1 (0.18) and exon 2  
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/codon\_start=1  
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/db\_xref="GI:862413"  
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GLPGHGAAPGGAAGARCLGFSARGFG"  
221..527  
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/number=2  
528..1017  
/gene="p16INK4/MTS1"  
/number=3  
BASE COUNT 215 a 297 c 291 g 214 t  
ORIGIN  
alignment\_scores:  
Quality: 553.50 Length: 174  
Ratio: 4.358 Gaps: 2  
Percent Similarity: 72.989 Percent Identity: 66.092  
alignment\_block:  
US-09-016-869A-2 x HSU26727 ..



DEFINITION Sequence 13 from patent US 5739027.

ACCESSION AR001325

VERSION AR001325.1 GI:3963392

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131

/organism="unknown"

BASE COUNT 232 a 327 c 343 g 229 t

ORIGIN

alignment\_scores: Quality: 553.00 Length: 107

Ratio: 5.168 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-016-869A-2 x AR001325 ..

Align seg 1/1 to: AR001325 from: 1 to: 1131

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66

332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

382 CGGCGCGAGCGCAACACGCGCGACCGCCACTCTCACCAGCCCGTGC 431

83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531

116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

532 CCTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCG 581

133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149

582 CTGCGGGGGGCCACGAGGCGAGTAAACCATGCCCGCATAGATGCCCGGAA 631

150 GlyProSerAspIleProAsp 156

632 GGTCCCTCAGACATCCCGAT 652

seq\_name: gb\_pat:AR037505

seq\_documentation\_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 13 from patent US 5801236.

ACCESSION AR037505

VERSION AR037505.1 GI:5955361

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131

/organism="unknown"

BASE COUNT 232 a 327 c 343 g 229 t

ORIGIN

alignment\_scores: Quality: 553.00 Length: 107

Ratio: 5.168 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-016-869A-2 x AR037505 ..

Align seg 1/1 to: AR037505 from: 1 to: 1131

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66

332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

382 CGGCGCGAGCGCAACACGCGCGACCGCCACTCTCACCAGCCCGTGC 431

83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531

116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

532 CCTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCG 581

133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149

582 CTGCGGGGGGCCACGAGGCGAGTAAACCATGCCCGCATAGATGCCCGGAA 631

150 GlyProSerAspIleProAsp 156

632 GGTCCCTCAGACATCCCGAT 652

seq\_name: gb\_pat:AR037505

seq\_documentation\_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 13 from patent US 5801236.

ACCESSION AR037505

VERSION AR037505.1 GI:5955361

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131

/organism="unknown"

BASE COUNT 232 a 327 c 343 g 229 t

ORIGIN

alignment\_scores: Quality: 553.00 Length: 107

Ratio: 5.168 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-016-869A-2 x AR037505 ..

Align seg 1/1 to: AR037505 from: 1 to: 1131

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66

332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

382 CGGCGCGAGCGCAACACGCGCGACCGCCACTCTCACCAGCCCGTGC 431

83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531

116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

532 CCTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCG 581

133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149

582 CTGCGGGGGGCCACGAGGCGAGTAAACCATGCCCGCATAGATGCCCGGAA 631

150 GlyProSerAspIleProAsp 156

632 GGTCCCTCAGACATCCCGAT 652

seq\_name: gb\_pat:AR037505

seq\_documentation\_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 13 from patent US 5801236.

ACCESSION AR037505

VERSION AR037505.1 GI:5955361

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131

/organism="unknown"

BASE COUNT 232 a 327 c 343 g 229 t

ORIGIN

alignment\_scores: Quality: 553.00 Length: 107

Ratio: 5.168 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-016-869A-2 x AR037505 ..

Align seg 1/1 to: AR037505 from: 1 to: 1131

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66

332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

382 CGGCGCGAGCGCAACACGCGCGACCGCCACTCTCACCAGCCCGTGC 431

83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531

116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

532 CCTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCG 581

133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149

582 CTGCGGGGGGCCACGAGGCGAGTAAACCATGCCCGCATAGATGCCCGGAA 631

150 GlyProSerAspIleProAsp 156

632 GGTCCCTCAGACATCCCGAT 652

seq\_name: gb\_pat:AR037505

seq\_documentation\_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 13 from patent US 5801236.

ACCESSION AR037505

VERSION AR037505.1 GI:5955361

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131

/organism="unknown"

BASE COUNT 232 a 327 c 343 g 229 t

ORIGIN

alignment\_scores: Quality: 553.00 Length: 107

Ratio: 5.168 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-016-869A-2 x AR037505 ..

Align seg 1/1 to: AR037505 from: 1 to: 1131

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66

332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

382 CGGCGCGAGCGCAACACGCGCGACCGCCACTCTCACCAGCCCGTGC 431

83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531

116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

532 CCTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCG 581

133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149

582 CTGCGGGGGGCCACGAGGCGAGTAAACCATGCCCGCATAGATGCCCGGAA 631

150 GlyProSerAspIleProAsp 156

632 GGTCCCTCAGACATCCCGAT 652

seq\_name: gb\_pat:AR037505

seq\_documentation\_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 13 from patent US 5801236.

ACCESSION AR037505

VERSION AR037505.1 GI:5955361

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131

/organism="unknown"

BASE COUNT 232 a 327 c 343 g 229 t

ORIGIN

alignment\_scores: Quality: 553.00 Length: 107

Ratio: 5.168 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-016-869A-2 x AR037505 ..

Align seg 1/1 to: AR037505 from: 1 to: 1131

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66

332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

382 CGGCGCGAGCGCAACACGCGCGACCGCCACTCTCACCAGCCCGTGC 431

83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531

116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

532 CCTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCG 581

133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149

582 CTGCGGGGGGCCACGAGGCGAGTAAACCATGCCCGCATAGATGCCCGGAA 631

150 GlyProSerAspIleProAsp 156

632 GGTCCCTCAGACATCCCGAT 652

seq\_name: gb\_pat:AR037505

seq\_documentation\_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 13 from patent US 5801236.

ACCESSION AR037505

VERSION AR037505.1 GI:5955361

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1..1131







241 CCCGAGCCCACTGCGCGGACCCCGCCACTCTCACCAGCCCGTGCAG 290  
 84 spAlaAArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
 291 ACGCTGCCCGGAGGCTCTCTGGACACGCTGGTGTCTGCACCGGCC 340  
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
 341 GGGGCGCGCTGGAGCTGCGGATCCCTGGGCGCTCTGCCGTGACCT 390  
 117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134  
 391 GGCTGAGAGCTGGCCATCGCATGTGCACGGTACTGCGCGGGCTG 440  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 441 CGGGGGCACCAGAGCGAGTACCATGCCCGCATAGATGCCGCGAAGT 490  
 151 ProSerAspIleProAsp 156  
 491 CCTCAGACATCCCGAT 508

seq\_name: N\_Geneseq\_36:T00747

seq\_documentation\_block:

AC T00747 standard; cDNA; 947 BP.

DT 08-MAY-1996 (first entry)

DE Multiple tumour suppressor 1 (MTS1) cDNA.

KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;

KW predisposition; melanoma; leukaemia; lymphoma; prognosis;

KW pancreas; breast; thyroid; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT misc\_feature 151

FT /\*tag= a

FT /note= "splice site acceptor"

FT misc\_feature 458

FT /\*tag= b

FT /note= "splice site acceptor"

FT FT

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Align seg 1/1 to: T00747 from: 1 to: 947

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17  
 1 ATGGAGCCGCGCGGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGC 50  
 17 aThrAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluAla 34  
 51 CACGCGCGCGCGCGGGTTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100  
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
 101 CGGTGGCGCTGCCCAACGACCCGAATAGTTACGGTCGGAGGCCGATCCAG 150  
 51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGln 67  
 151 GTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTGCTCCACGG 200  
 67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis 84  
 201 CGCGAGCCCAACTGCGCGCCGACCCCGCACTCTCACCGACCCGTCACG 250  
 84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
 251 ACGTGGCGGGAGGGCTTCTGGACACGCTGGTGGTGGTGGTGGTGGTGG 300  
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
 301 GGGCGCGGCTGGACGTGCGCGATGCTGGGCGCTGTCGCCGTGGACCT 350  
 117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134  
 351 GGCTGAGAGCTGGGCGCATCGCATGTGCACGCTACCTGCGCGCGCTG 400  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 401 CGGGGGCACCAGAGGAGCATACCATGCCCGCATAGATGCCCGGAGAGT 450  
 151 ProSerAspIleProAsp 156  
 451 CCTCAGACATCCCGAT 468

seq\_name: N\_Geneseq\_36:V11238

seq\_documentation\_block:

ID V11238 standard; cDNA; 471 BP.

AC V11238;

DE Human MTS1 cDNA.

DE 15-JUL-1998 (first entry)

KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;

KW familial melanoma locus; MLM; predisposition; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..471

FT /\*tag= a

FT /product= MTS1

FT /note= "multiple tumour suppressor"

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-250421/22.

DR P-PSDB; W40524.

PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are

PT useful for the diagnosis of cancers related to MTS1E1-beta

alignment\_scores:  
 Quality: 796.00 Length: 156  
 Ratio: 5.103 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.359

alignment\_block:

US-09-016-869A-2 x T00747

Sequence 947 BP; 207 A; 271 C; 273 G; 196 T;  
 Detecting polymorphism associated with cancer pre:disposition - also  
 DNA, vectors and host cells e.g. for gene or protein replacement  
 therapy and drug screening  
 PS Disclosure; Pages 111-112; 148pp; English.  
 CC An individual can be diagnosed as having a predisposition to cancer  
 CC by detecting an alteration in the wild type multiple tumour  
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1  
 CC cDNA T00747. The above assay can also be used in the diagnosis and  
 CC prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and  
 CC thyroid cancers, etc.

PT mutation(s) and their treatment

PS Disclosure: Column 61-62: 72bp; English.  
 CC This cDNA sequence encodes a human multiple tumour suppression protein,  
 CC MTS1. The MTS gene locus is also referred to as the familial melanoma  
 CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations  
 CC in MTS genes can be used in the diagnosis of predisposition to cancers,  
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,  
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,  
 CC ovary, uterus, testis, kidney, stomach and rectum.  
 SQ Sequence 471 BP: 68 A; 153 C; 186 G; 64 T;

alignment\_scores:  
 Quality: 789.00 Length: 156  
 Ratio: 5.090 Gaps: 0  
 Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x V11238 ..

Align seg 1/1 to: V11238 from: 1 to: 471

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17  
 |||:::|||||  
 1 ATGGAGCGCGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGGC 50  
 17 aThrAlaAlaAArgGlyArgValGluGluValAlaArgAlaLeuGluA 34  
 |||:::|||||  
 51 CACGGCGCGCGCGGGTGGGTAGAGGAGTGGCGGCGCTGCTGGAGG 100  
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
 |||:::|||||  
 101 CGGGGGCGCTGCCCAACGACCGCAATAGTTACGGTCGGAGCGCATCCAG 150  
 51 ValMetMetGlySerAlaAArgValAlaGluLeuLeuLeuHisG1 67  
 |||:::|||||  
 151 GTCATGATGATGGCAGCGCGGAGTGGCGGAGCTGCTGCTCCACGG 200  
 67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
 |||:::|||||  
 201 CGGGAGCCCAACTGCGCGCAGCCCGCCACTCTCACCAGCCCGTGCACG 250  
 84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
 |||:::|||||  
 251 ACCTGTAGGAGCTGGGCCATCGCATGTCGACACGCTGGTGGTGCACCGGCC 300  
 101 GlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValAspLe 117  
 |||:::|||||  
 301 GGGCGCGGCTGGACGTGCGGATGCTGGGCGCTGCTGCCCGTGACCT 350  
 117 uAlaGluGluLeuGlyHisArgAspValAlaAArgTyrLeuArgAlaAla 134  
 |||:::|||||  
 351 GGCTGAGGAGCTGGGCCATCGCATGTCGACACGCTACCTGCGCGGCTG 400  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 |||:::|||||  
 401 CGGGGGCCAGCAGGAGGAGTAAACATGCCGCATAGATGCCGCGGAAGGT 450  
 151 ProSerAspIleProAsp 156  
 |||:::|||||  
 451 CCCTCAGACATCCCGAT 468

seq\_name: N\_Geneseq\_36:V53819

seq\_documentation\_block:

ID V53819 standard; CDNA: 471 BP.

AC V53819;

DE 04-DEC-1998 (first entry)

DT Nucleotide sequence of the CDS of the multiple tumour suppressor 1.

KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;

OS somatic mutation; gene therapy; ds.

OS Homo sapiens.

FT Key Location/Qualifiers

CDS 1..471  
 /\*tag= a  
 /product= "human MTS-1"

US5801236-A.  
 01-SEP-1998.  
 07-JUN-1995; 480810.  
 07-JUN-1995; US-480810.  
 18-MAR-1994; US-214582.  
 18-MAR-1994; US-215086.  
 18-MAR-1994; US-215087.  
 14-APR-1994; US-227369.  
 01-JUN-1994; US-251938.  
 17-MAR-1995; WO-U03316.  
 (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR WPI: 98-494842/42.  
 P-PSDB: W74549.  
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
 useful as hybridisation probes, primers and recombinant production  
 of MTS in the diagnosis and treatment of cancers related to MTS  
 PT mutation(s)  
 PS Claim 1: Column 61-62: 73bp; English.  
 CC This is the nucleotide sequence of the multiple tumour suppressor 1  
 CC (MTS-1) gene, used in the method of the invention. The MTS gene  
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
 CC standard nucleic hybridisation techniques, of patient samples. The  
 CC mutated sequences are those that are present in somatic mutations  
 CC of the gene in cancers. The vectors can be used for gene therapy  
 CC strategies to replace function of mutated protein in patients. These  
 CC can also be used to construct protein mimetics, also for therapeutic  
 CC strategies. In addition the expression constructs can also be used  
 CC for recombinant production of MTS. Recombinant MTS can be used to  
 CC screen for drugs to be used for cancer therapy, and the protein  
 CC itself may also be used to restore MTS function in a cell.  
 SQ Sequence 471 BP: 68 A; 153 C; 186 G; 64 T;

alignment\_scores:

Quality: 789.00 Length: 156  
 Ratio: 5.090 Gaps: 0  
 Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x V53819 ..

Align seg 1/1 to: V53819 from: 1 to: 471

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17  
 |||:::|||||  
 1 ATGGAGCGCGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGGC 50  
 17 aThrAlaAlaAArgGlyArgValGluGluValAlaArgAlaLeuGluA 34  
 |||:::|||||  
 51 CACGGCGCGCGCGGGTGGGTAGAGGAGTGGCGGCGCTGCTGGAGG 100  
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
 |||:::|||||  
 101 CGGGGGCGCTGCCCAACGACCGCAATAGTTACGGTCGGAGCGCATCCAG 150  
 51 ValMetMetGlySerAlaAArgValAlaGluLeuLeuLeuHisG1 67  
 |||:::|||||  
 151 GTCATGATGATGGCAGCGCGGAGTGGCGGAGCTGCTGCTCCACGG 200  
 67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
 |||:::|||||  
 201 CGGGAGCCCAACTGCGCGCAGCCCGCCACTCTCACCAGCCCGTGCACG 250  
 84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
 |||:::|||||  
 251 ACCTGTAGGAGGCTTCCTGGACACGCTGGTGGTGGTGCACCGGCC 300  
 101 GlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValAspLe 117  
 |||:::|||||

301 GGGGGCGGCTGCGACGTCGGCGGATCCCTGGGGCCGCTGCGCGTGGACCT 350  
 117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134  
 351 GGCTGAGGAGCTGGCCATCGCGATGTCGACGGTACCTGCGCGGGCTG 400  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 401 CGGGGGGACCAAGAGCAGTACCATGCCGCGATAGATGCCGCGGAAGT 450  
 151 ProSerAspIleProAsp 156  
 451 CCTCAGACATCCCCGAT 468

seq\_name: N\_Geneseq\_36:V70583

seq\_documentation\_block:

ID V70583 standard; cDNA; 471 BP.

AC V70583;

DE 03-FEB-1999 (first entry)

DE cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.

KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..471

FT 150..151

FT /\*tag= a

FT /\*tag= b

FT /note= "splice site"

FT 478..458

FT /\*tag= c

FT /note= "splice site"

FT US5843756-A.

PN 01-DEC-1998.

PD 28-JUL-1995; 058735.

PF 28-JUL-1995; US-508735.

PR 07-JUN-1995; US-487033.

PA (MIRI-) MYRIAD GENETICS INC.

PI Jiang P, Kamb A, Stone S;

DR WPI; 99-044585/04.

DR P-PSDB; W80524.

PT Mouse multiple tumour suppressor gene segment - useful for primer

PT design

PS Disclosure; Columns 63-66; 80pp; English.

CC The present sequence encodes a human multiple tumour suppressor 1

CC (MTS1) protein. The sequence is homologous to the corresponding

CC murine gene. Primers designed from the gene can be used to design

CC primers to detect abnormalities i.e. polymorphisms which may

CC predispose towards malignancies such as melanoma, leukaemia,

CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,

CC thyroid, pancreas, uterus and kidneys.

CC Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;

SQ

alignment\_scores:

Quality: 789.00 Length: 156

Ratio: 5.090 Gaps: 0

Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x V70583

Align seg 1/1 to: V70583 from: 1 to: 471

1 MetAspProAlaAlaGlySerMetGluProSerAlaAspTyrLeuAl 17

1 ATGGAGCCGGCGGGGAGCAGCAGTGGAGCCCTCGCTGACTGGCTGGC 50

17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34

51 CACGCCCGCGGGGTCGGTACGAGGAGTGGCGGCTGCTGGAGG 100

34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50

117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134  
 351 GGCTGAGGAGCTGGCCATCGCGATGTCGACGGTACCTGCGCGGGCTG 400  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 401 CGGGGGGACCAAGAGCAGTACCATGCCGCGATAGATGCCGCGGAAGT 450  
 151 ProSerAspIleProAsp 156  
 451 CCTCAGACATCCCCGAT 468

seq\_name: N\_Geneseq\_36:T72311

seq\_documentation\_block:

ID T72311 standard; cDNA; 947 BP.

AC T72311;

DT 10-SEP-1997 (first entry)

DE Human multiple tumour suppressor gene 1.

KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..471

FT /\*tag= a

FN US5624819-A.

PD 29-APR-1997.

PF 18-MAR-1994; 214582.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-U03537.

PR 07-JUN-1995; US-474177.

PA (MYRI-) MYRIAD GENETICS INC.

PA (UTAH) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

PI WPI; 97-258217/23.

DR P-PSDB; W19251.

PT Human mutant multiple tumour suppressor gene sequences - for

PT production of recombinant mutant polypeptide(s)

PS Claim 1; Columns 87-90; 72pp; English.

CC The present sequence the human multiple tumour suppressor gene 1

CC (MTS1), useful in cancer diagnosis.

SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment\_scores:

Quality: 789.00 Length: 156

Ratio: 5.090 Gaps: 0

Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x T72311

Align seg 1/1 to: T72311 from: 1 to: 947

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1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
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1 ATGGAGCGCGCGGGAGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGC 50
|||||
17 aThAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluA 34
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51 CACGGCGCGCGCGGGGTGGGTAGAGAGGTGCGGCGCTGCTGGAGG 100
|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
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101 CGGGGGCGCTGCCACGCCAGCATAGTTACGGTCGGAGGCCATCCAG 150
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51 ValMetMetGlySerAlaAlaArgValAlaGluLeuLeuLeuHisG1 67
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151 GTCATGATGATGGCAGCGCGGAGTGGCGAGCTGCTGCTGCCACGG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||
201 CGCGAGCCCAACTGCGCGGACCGCCGCACTCTCACCGAGCCCGTGACG 250
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84 spAlaAlaAlaArgGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
251 ACGTGTCCCGGGAGGGTCTCTGGACACGCTGGTGGTCTGCACCGGCC 300
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101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
301 GGGCGCGGCTGGACGTGCGGATGCTGCGGCGCTGCTGCCGCTGGACCT 350
|||||
117 uAlaGluLeuLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
|||||
351 GGCTGAGGAGCTGGCGCATCCGATGTCGCACGCTACCTGCGCGCGCTG 400
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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401 CGGGGGCCACGAGAGGAGTACCATGCCCGCATAGATGCCCGCGGAGGT 450
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451 CCCTCAGACATCCCGAT 468
|||||

```

seq\_name: N\_Geneseq\_36.V11270

seq\_documentation\_block:

ID V11270 standard; cDNA; 947 BP.  
 DT 15-JUL-1998 (first entry)  
 DE Human MTS1 cDNA variant.  
 KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;  
 KW familial melanoma locus; MLM; predisposition; ds.  
 OS Homo sapiens.

FT	Key	Location/Qualifiers
FT	misc_feature	151
FT		/tag= a
FT		/note= "splice site acceptor"
FT	misc_feature	458
FT		/tag= b
FT		/note= "splice site acceptor"

US5739027-A.  
 PD 14-APR-1998.  
 PF 07-JUN-1995; 487033.  
 PR 07-JUN-1995; US-487033.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03316.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR WPI; 98-250421/22.

PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are  
 PT useful for the diagnosis of cancers related to MTS1E1-beta  
 PT mutation(s) and their treatment  
 PS Disclosure; Column 89-90; 72pp; English.  
 CC This cDNA sequence encodes a variant of the human multiple tumour  
 CC suppression protein, MTS1. The MTS gene locus is also referred to as the  
 CC familial melanoma (MLM) gene locus, located on human chromosome 9p21.  
 CC germ line mutations in MTS genes can be used in the diagnosis of  
 CC predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma,  
 CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of  
 CC the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach  
 CC and rectum.  
 SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment\_scores:

Quality	Length
Ratio: 789.00	156
Percent Similarity: 99.359	Gaps: 0
	Percent Identity: 98.718

alignment\_block:

US-09-016-869A-2 x V11270 ..

Align seg 1/1 to: V11270 from: 1 to: 947

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1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
|||||
1 ATGGAGCGCGCGGGAGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGC 50
|||||
17 aThAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluA 34
|||||
51 CACGGCGCGCGCGGGGTGGGTAGAGAGGTGCGGCGCTGCTGGAGG 100
|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|||||
101 CGGGGGCGCTGCCACGCCAGCATAGTTACGGTCGGAGGCCATCCAG 150
|||||
51 ValMetMetGlySerAlaAlaArgValAlaGluLeuLeuLeuHisG1 67
|||||
151 GTCATGATGATGGCAGCGCGGAGTGGCGAGCTGCTGCTGCCACGG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||
201 CGCGAGCCCAACTGCGCGGACCGCCGCACTCTCACCGAGCCCGTGACG 250
|||||
84 spAlaAlaAlaArgGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
251 ACGTGTCCCGGGAGGGTCTCTGGACACGCTGGTGGTCTGCACCGGCC 300
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101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
301 GGGCGCGGCTGGACGTGCGGATGCTGCGGCGCTGCTGCCGCTGGACCT 350
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117 uAlaGluLeuLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
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351 GGCTGAGGAGCTGGCGCATCCGATGTCGCACGCTACCTGCGCGCGCTG 400
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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401 CGGGGGCCACGAGAGGAGTACCATGCCCGCATAGATGCCCGCGGAGGT 450
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151 ProSerAspIleProAsp 156
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451 CCCTCAGACATCCCGAT 468
|||||

```

seq\_name: N\_Geneseq\_36.V53851

seq\_documentation\_block:

ID V53851 standard; cDNA; 947 BP.  
 AC V53851;  
 DT 04-DEC-1998 (first entry)  
 DE Coding sequence 3 of the multiple tumour suppressor 1.  
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;

KW somatic mutation; gene therapy; ds.  
OS Homo sapiens.  
PN US5801236-A.  
PD 01-SEP-1998.  
PF 07-JUN-1995; 480810.  
PR 07-JUN-1995; US-480810.  
PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215087.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PR 17-MAR-1995; WO-U03316.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Kamb A;  
DR WPI; 98-494842/42.  
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
PS Claim 1; Fig 17; 73pp; English.  
CC This is the nucleotide sequence of the multiple tumour suppressor 1  
CC (MTS-1) gene, used in the method of the invention. The MTS gene  
CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
CC standard nucleic hybridisation techniques, of patient samples. The  
CC mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.  
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
US-09-016-869A-2 x V53851 ..

Align seg 1/1 to: V53851 from: 1 to: 947

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1 ATGGAGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCG 50  
|||||  
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34  
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51 CACGGCGCGCGCGGGTTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100  
|||||  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
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101 CGGGGGCGCTGCCACACCGACGATAGTTCGGTGGAGCGGATCCAG 150  
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51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
|||||  
151 GTCATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCACGG 200  
|||||  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
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201 CGCGGAGCCCAACTCGCGCGGACCCGCCCACTCTCACCCGACCGGTG 250  
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84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
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|||||  
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
|||||  
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|||||

117 uAlaGluLeuLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134  
|||||  
351 GGCTGAGGAGCTGGGCCATCGCATGTCCACGGTACCTGCGCGCGGTG 400  
|||||  
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
|||||  
401 CGGGGGCGCACGAGGCGCAGTACCATGCCCATAGATGCCCGCGGAAGT 450  
|||||  
151 ProSerAspIleProAsp 156  
|||||  
451 CCTCTCAGACATCCCGCAT 468

seq\_name: N\_Geneseq\_36.V70615

seq\_documentation\_block:  
ID V70615 standard; cDNA; 947 BP.  
AC V70615;  
DT 03-FEB-1999 (first entry)  
DE cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.  
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT misc\_feature 151  
FT /tag= a  
FT /note= "splice site acceptor"  
FT misc\_feature 458  
FT /tag= b  
FT /note= "splice site acceptor"  
FT US5843756-A.  
PN 01-DEC-1998.  
PD 28-JUL-1995; 058735.  
PR 28-JUL-1995; US-508735.  
PR 07-JUN-1995; US-487033.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Jiang P, Kamb A, Stone S;  
DR WPI; 99-044585/04.  
PT Mouse multiple tumour suppressor gene segment - useful for primer  
PT design  
PS Disclosure; Fig 17; 80pp; English.  
CC The present sequence represents the cDNA sequence for a human multiple  
CC tumour suppressor 1 (MTS1) gene, including noncoding portions. The gene  
CC can be used to design primers to detect abnormalities i.e. polymorphisms  
CC which may predispose towards malignancies such as melanoma, leukaemia,  
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,  
CC thyroid, pancreas, uterus and kidneys.  
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment\_scores:  
Quality: 789.00 Length: 156  
Ratio: 5.090 Gaps: 0  
Percent Similarity: 99.359 Percent Identity: 98.718

alignment\_block:  
US-09-016-869A-2 x V70615 ..

Align seg 1/1 to: V70615 from: 1 to: 947

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51 CACGGCGCGCGCGGGTTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100  
|||||  
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
|||||  
101 CGGGGGCGCTGCCACACCGACGATAGTTCGGTGGAGCGGATCCAG 150  
|||||  
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
|||||  
151 GTCATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCACGG 200  
|||||  
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
|||||  
201 CGCGGAGCCCAACTCGCGCGGACCCGCCCACTCTCACCCGACCGGTG 250  
|||||  
84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
|||||  
251 AGCTGCCCCGGAGGGCTTCCTGGACACCGCTGTGTGCTGCCCGGGCC 300  
|||||  
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
|||||  
301 GGGCGCGCGCTGGCGTGGCGATGCTGCGGGCCGCTCTGCCCGTGGACCT 350  
|||||

67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
 201 CGGGAGCCCACTCGCGGACCGCCCACTCTCACCCGACCGGTGCACG 250  
 84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
 251 ACCTGCCCGGGAGGCTCTCTGCACACGCTGGTGTCTGCACCGGGCC 300  
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
 301 GGGCGCGGCTGCACGCTGCGCGATGCTGGGCGCTCTGCGCGGTGACCT 350  
 117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134  
 351 GGTGAGGAGCTGGGCGATGCGCATGTGCGACGTTACCTGCGGCGGCTG 400  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 401 CGGGGGCCACAGGAGTAACTATGCCGCGATAGATGCCCGCGGAGGT 450  
 151 ProSerAspIleProAsp 156  
 451 CCCTCAGACATCCCGAT 468

seq\_name: N\_Geneseq\_36:T60951

seq\_documentation\_block:  
 AC T60951 standard; DNA; 987 BP.  
 DT 28-OCT-1997 (first entry)  
 DE Tumour suppressor p16 coding sequence.  
 KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;  
 KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;  
 KW anti-angiogenic activity; hyperproliferative disorder; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 41..511  
 FT /\*tag= a  
 FT /product= Tumour suppressor p16  
 PN WO9703635-A2.  
 PD 06-FEB-1997.  
 PF 17-JUL-1996; U11787.  
 PR 17-JUL-1995; US-502881.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PI Jin X, Roth J;  
 DR WPI: 97-132336/12.  
 P-PSDB: W10627.  
 PT Expression construct contg. DNA for tumour suppressor p16 - to  
 PT restore p16 activity to transformed cells, useful for treating lung  
 PT or bladder cancer or melanoma  
 PS Disclosure: Fig 1a; 92pp: English.  
 CC This sequence represents the coding sequence for the tumour suppressor  
 CC p16. This sequence is joined to a promoter functional in eukaryotic cells  
 CC and used in the expression construct of the invention. p16 is an  
 CC inhibitory subunit, which is involved in the control of cyclin-dependent  
 CC kinase 4 activity, and functions as a tumour suppressor. By detecting  
 CC this sequence or the encoded protein, cancer cells can be detected. When  
 CC the nucleic acid molecule is in the sense orientation, the expression  
 CC construct can be used to restore p16 function in a cell, particularly by  
 CC reversing the transformed phenotype in tumours, especially lung or  
 CC bladder cancer or melanoma. It may also have anti-angiogenic activity,  
 CC and inhibit hyperproliferative disorders, e.g. restenosis. When the  
 CC nucleic acid molecule is inserted in the antisense orientation, the  
 CC expression construct inhibits p16 function. Reduced or increased levels  
 CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by  
 CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting  
 CC or immunoassay.  
 SQ Sequence 987 BP: 219 A: 279 C: 295 G: 194 T;

alignment\_scores: Quality: 789.00 Length: 156

Ratio: 5.090 Gaps: 0  
 Percent Similarity: 99.359 Percent Identity: 98.718  
 alignment\_block:  
 US-09-016-869A-2 x T60951 ..  
 Align seg 1/1 to: T60951 from: 1 to: 987  
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 17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34  
 91 CAGGCGCGCGCGCGGGTGGGTAGAGAGGTGCGGCGCTGCTGCTGGAGG 140  
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
 141 CGGGGGCGCTGCCCAACGACCGCAATAGTTACGGTCGGAGCGCGATCCAG 190  
 51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67  
 191 GTCATGATGATGGCAGCGCGCGAGTGGCGGAGCTGCTGCTGCTCCACGG 240  
 67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84  
 241 CGCGGAGCCCACTGCGCGGACCGCCCACTCTCACCCGACCGGTGCACG 290  
 84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100  
 291 ACCTGCCCGGGAGGCTCTCTGCACACGCTGGTGTCTGCACCGGGCC 340  
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117  
 341 GGGCGCGGCTGCACGCTGCGCGATGCTGGGCGCTCTGCGCGGTGACCT 390  
 117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134  
 391 GGCTGAGGAGCTGGGCGATGCGCATGTGCGACGTTACCTGCGCGGCTG 440  
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150  
 441 CGGGGGCCACAGGAGTAACTATGCCGCGATAGATGCCCGCGGAGGT 490  
 151 ProSerAspIleProAsp 156  
 491 CCCTCAGACATCCCGAT 508

seq\_name: N\_Geneseq\_36:X26233

seq\_documentation\_block:  
 ID X26233 standard; DNA; 737 BP.  
 AC X26233;  
 DT 25-MAY-1999 (first entry)  
 DE Truncated p27/p16 fusion protein encoding DNA.  
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerosis; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16; truncated; ss.  
 OS Homo sapiens.  
 PN WO9906540-A2.  
 PD 11-FEB-1999.  
 PF 29-JUL-1998; U15759.  
 PR 29-JUL-1997; US-902572.  
 PA (MITO-) MITOPIX INC.  
 PI Beach DH, Gyuris J, Lamphere L;  
 DR WPI: 99-153770/13.  
 P-PSDB: W95105.  
 PT Fusion and chimaeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and

PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration  
 PS Claim 60; Page 84-85; 88pp; English.  
 CC The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,  
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)  
 CC second gene construct comprising a sequence encoding a polypeptide that  
 CC promotes endothelialisation, and (iii) a gene delivery composition for  
 CC delivering the GCs to a cell for transfection. Also provided are nucleic  
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic  
 CC polypeptide sequence (TP) from an intracellular protein that alters a  
 CC cellular process when FP enters the cell, and (ii) a transcellular  
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
 CC consists of at least one CDK-binding motif and a TCP. See X26220 for  
 CC detailed uses of the recombinant transfection system. The present  
 CC sequence represents a DNA encoding a human truncated p27/p16 fusion  
 CC protein.  
 SQ Sequence 737 BP; 135 A; 227 C; 267 G; 108 T;

alignment\_scores:  
 Quality: 788.00 Length: 155  
 Ratio: 5.117 Gaps: 0  
 Percent Similarity: 99.355 Percent Identity: 99.355  
 alignment\_block:  
 US-09-016-869A-2 x X26233

Align seg 1/1 to: X26233 from: 1 to: 737

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 262 GATCGCGCGGGGAGCAGCATGGAGCTTCGGCTGACTGCTGCCAC 311  
 18 rAlaAlaAlaArgGlyArgValGluValArgAlaLeuGluAla1av 35  
 312 GCGCGCGCGGGGTCGGGTAGAGAGGTGGCGGCTGCTGGAGGCG 361  
 35 AlAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51  
 362 GGGCGCTGCCCAACGACCGATAGTACGTCGGAGGCCGATCCAGGTC 411  
 52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68  
 412 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGCGGC 461  
 68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85  
 462 GGAGCCCACTCGCGGACCCCGCCACTCTCACCGACCCGTCGACGAG 511  
 85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101  
 512 CTGCGCGGGAGGGCTTCTGGACAGCTGGTGGTGGTCCACCGCGCGG 561  
 102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118  
 562 GCGCGCTGACGATGCGCGATGCTGGGCGCTCTGCCGCTGGACCTGCG 611  
 118 aGluLeuLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 135  
 612 TGAGAGAGCTGGGCCATCGCGATGTCGACGGTACCTGCGCGGGCTGCG 661  
 135 lYgLYThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGlyPro 151  
 662 GGGGACACAGAGCAGTACCAATGCCCGATAGATGCCCGGAGGTCC 711  
 152 SerAspIleProAsp 156  
 712 TCAGACATCCCGAT 726

seq\_name: N\_Geneseq\_36:X26234

seq\_documentation\_block:

ID X26234 standard; DNA; 782 BP.  
 AC X26234;  
 DT 25-MAY-1999 (first entry)  
 DE Truncated p27/p16 fusion protein encoding DNA.  
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16; truncated; ss.  
 OS Homo sapiens.  
 PN WO9006540-A2.  
 PD 11-FEB-1999.  
 PF 29-JUL-1998; U15759.  
 PR 29-JUL-1997; US-902572.  
 PA (MITO-) MITOTIX INC.  
 PI Beach DH, Gyuris J, Lamphere L;  
 DR WPI; 99-153770/13.  
 DR P-PSDB; W95106.  
 PT Fusion and chimaeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration  
 PS Claim 60; Page 85; 88pp; English.  
 CC The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,  
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)  
 CC second gene construct comprising a sequence encoding a polypeptide that  
 CC promotes endothelialisation, and (iii) a gene delivery composition for  
 CC delivering the GCs to a cell for transfection. Also provided are nucleic  
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic  
 CC polypeptide sequence (TP) from an intracellular protein that alters a  
 CC cellular process when FP enters the cell, and (ii) a transcellular  
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
 CC consists of at least one CDK-binding motif and a TCP. See X26220 for  
 CC detailed uses of the recombinant transfection system. The present  
 CC sequence represents a DNA encoding a human truncated p27/p16 fusion  
 CC protein.  
 SQ Sequence 782 BP; 137 A; 236 C; 295 G; 114 T;

alignment\_scores:

Quality: 788.00 Length: 155  
 Ratio: 5.117 Gaps: 0  
 Percent Similarity: 99.355 Percent Identity: 99.355

alignment\_block:

US-09-016-869A-2 x X26234

Align seg 1/1 to: X26234 from: 1 to: 782

2 AspProAlaAlaGlySerMetGluProSerAlaAspTrpLeuAla18  
 307 GATCGCGCGGGGAGCAGCATGGAGCTTCGGCTGACTGCTGCCAC 356  
 18 rAlaAlaAlaArgGlyArgValGluValArgAlaLeuGluAla1av 35  
 357 GCGCGCGCGGGGTCGGGTAGAGAGGTGGCGGCTGCTGGAGGCG 406  
 35 AlAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51  
 407 GGGCGCTGCCCAACGACCGATAGTACGTCGGAGGCCGATCCAGGTC 456  
 52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68  
 457 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGCGGC 506



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68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
507 GGAGCCCAACTGGCGCCAGCCCGCACTCTCACCCGACCCGCTGCACGACG 556
85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
557 CTGCCGGGAGGGCTTCTTGGACACGCTGTGTGTGTGTGTGTGTGTGTGT 606
102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
607 GCAGCGGTGACGCTGCGCGATGCTGTGGCGCGCTGTGTGTGTGTGTGTGT 656
118 aGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaAG 135
657 TGAGGAGCTGGGCAATCGCATGTCGACACGTCACCTGCGCGCGCTGCGG 706
135 lyGlyThrArgGlySerAsnHisAlaArgTleAspAlaAlaGluGlyPro 151
707 GGGCACCAAGGACGATACCATGCGCGCATAGATGCGCGGAGGTGCC 756
152 SerAspIleProAsp 156
757 TCAGACATCCCGAT 771
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seq\_name: N\_Geneseq\_36.X26231

seq\_documentation\_block:

ID X26231 standard; DNA; 1028 BP.

AC X26231;

DE Truncated p27/p16 fusion protein encoding DNA.

KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
KW tachycardia; human; p27; p16; truncated; ss.

OS Homo sapiens.

PN WO906540-A2.

PD 11-FEB-1999.

PF 29-JUL-1998; U15759.

PR 29-JUL-1997; US-902572.

PA (MITO-) MITOTIX INC.

PI Beach DH, Gyuris J, Lamphere L;

WPI: 99-153770/13.

DR P-PSDB; W95103.

PT Fusion and chimaeric proteins including cyclin-dependent kinase

binding motif - used for regulation of cell proliferation and

differentiation, for treatment of, e.g. vascular injury, cancers,

PT fibrosis and neurodegeneration

PS Claim 60; Page 83; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases  
(CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
transfection system (A) that comprises: (i) first gene construct  
comprising a sequence encoding an inhibitory polypeptide containing at  
least one CDK-binding motif for binding and inhibiting activity of a CDK,  
linked to a transcription regulator functional in eukaryotic cells; (ii)  
second gene construct comprising a sequence encoding a polypeptide that  
promotes endothelialisation, and (iii) a gene delivery composition for  
delivering the Gcs to a cell for transfection. Also provided are nucleic  
acids encoding a fusion protein (FP) containing: (i) a therapeutic  
polypeptide sequence (TP) from an intracellular protein that alters a  
cellular process when FP enters the cell, and (ii) a transcellular  
polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
consists of at least one CDK-binding motif and a TCP. See X26220 for  
detailed uses of the recombinant transfection system. The present  
sequence represents a DNA encoding a human truncated p27/p16 fusion  
protein.

SQ

alignment\_scores:  
Quality: 788.00 Length: 155  
Ratio: 5.117 Gaps: 0  
Percent Similarity: 99.355 Percent Identity: 99.355

alignment\_block:

US-09-016-869A-2 x X26231

Align seg 1/1 to: X26231 from: 1 to: 1028

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18 rAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluAlav 35
603 GGCGCGCGCGCGGGTGGGTAGAGGAGGTGCGGCGCTGCTGGAGGCGG 652
35 aAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51
653 GGGCGCTGCCCCAACGACCAATAGTTACGTCGGAGCGCATCCAGGTC 702
52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68
703 ATGATGATGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCCACGCGC 752
68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
753 GGAGCCCAACTGGCGCGACCCCGCACTCTCACCCGACCCGCTGCACGACG 802
85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
803 CTGCCGGGAGGGCTTCTTGGACACGCTGTGTGTGTGTGTGTGTGTGTGT 852
102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
853 GCAGCGGTGACGCTGCGCGATGCTGTGGCGCGCTGTGTGTGTGTGTGTGT 902
118 aGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaAG 135
903 TGAGGAGCTGGGCAATCGCATGTCGACACGTCACCTGCGCGCGCTGCGG 952
135 lyGlyThrArgGlySerAsnHisAlaArgTleAspAlaAlaGluGlyPro 151
953 GGGCACCAAGGACGATACCATGCGCGCATAGATGCGCGGAGGTGCC 1002
152 SerAspIleProAsp 156
1003 TCAGACATCCCGAT 1017
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seq\_name: N\_Geneseq\_36.X26232

seq\_documentation\_block:

ID X26232 standard; DNA; 1073 BP.

AC X26232;

DE Truncated p27/p16 fusion protein encoding DNA.

KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
KW tachycardia; human; p27; p16; truncated; ss.

OS Homo sapiens.

PN WO906540-A2.

PD 11-FEB-1999.

PF 29-JUL-1998; U15759.

PR 29-JUL-1997; US-902572.

PA (MITO-) MITOTIX INC.

PI Beach DH, Gyuris J, Lamphere L;

WPI: 99-153770/13.

PT Fusion and chimaeric proteins including cyclin-dependent kinase

PT binding motif - used for regulation of cell proliferation and  
PT differentiation, for treatment of, e.g. vascular injury, cancers,  
PT fibrosis and neurodegeneration  
PS Claim 60: Page 83-84; 88pp; English.  
CC The invention relates to novel inhibitors of cyclin-dependent kinases  
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
CC transfection system (A) that comprises: (i) first gene construct  
CC comprising a sequence encoding an inhibitory polypeptide containing at  
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,  
CC linked to a transcription regulator functional in eukaryotic cells; (ii)  
CC second gene construct comprising a sequence encoding a polypeptide that  
CC promotes endothelialisation, and (iii) a gene delivery composition for  
CC delivering the GCS to a cell for transfection. Also provided are nucleic  
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic  
CC polypeptide sequence (TP) from an intracellular protein that alters a  
CC cellular process when FP enters the cell, and (ii) a transcellular  
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
CC consists of at least one CDK-binding motif and a TCP. See X26220 for  
CC detailed uses of the recombinant transfection system. The present  
CC sequence represents a DNA encoding a human truncated p21/p16 fusion  
CC protein.  
SQ Sequence 1073 BP; 215 A; 317 C; 388 G; 153 T;

alignment\_scores:  
Quality: 788.00 Length: 155  
Ratio: 5.117 Gaps: 0  
Percent Similarity: 99.355 Percent Identity: 99.355

alignment\_block:  
US-09-016-869A-2 x X26232 ..

Align seg 1/1 to: X26232 from: 1 to: 1073

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18 rAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluAlaV 35
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648 GCCCGCGCGCGGTCGGTAGAGAGGTGCGGCGCTGCTGGAGCGG 697

35 alAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51
|||||
698 GGGCGCTGCCCAACGACCGAATAGTACGTCGAGGCGCGATCCAGGTC 747

52 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAla 68
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748 ATGATGATGGGAGCGCCGAGTGCGGAGCTGCTGCTCCACGGCGC 797

68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
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798 GGAGCCCACTGCGCGAGCCCGCCACTCTCACCGACCGCTGCAGCAGC 847

85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
|||||
848 CTGCGCGGAGGGCTCTCTGGACAGCTGGTGTGTGACCGCGCGCGG 897

102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
|||||
898 GCGCGCTGGAGCTGGCGCATGCTTGGGCGCTGCTGCGCTGGAGCTGGC 947

118 aGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAlaAlaG 135
|||||
948 TCAGGAGCTGGCGCATCGGATGTCGACGGTACCTGCGCGCGCTGGCG 997

135 IyGlyThrArgGlySerAsnHisAlaArgIleAspAlaGluGlyPro 151
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998 GGGGACCAAGAGGAGTAACCATGCCCGCATAGATGCCCGGAAGTCCC 1047

152 SerAspIleProAsp 156
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seq\_name: N\_Geneseq\_36:T74053

seq\_documentation\_block:

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ID T74053 standard; cDNA; 1098 BP.
AC T74053;
DT 16-MAR-1998 (first entry)
DE CDK inhibitory fusion protein p16p27 coding sequence.
KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
KW chimeric polypeptide; human; binding motif; proliferation control;
KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
KW tissue degeneration; therapy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1098
FT /tag= a
FT WO9727297-A1.
PD 31-JUL-1997.
PF 17-JAN-1997; U00569.
PR 23-JAN-1996; US-589981.
PA (MITO-) MITOTIX INC.
PI Beach D, Gyuris J, Lamphere L;
DR WPI; 97-393685/36.
DR P-PSDB; W23536.
PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
PT therapy of cancer and other proliferative and differentiative
PT diseases
PS Claim 13; Page 46-48; 58pp; English.
CC This sequence encodes a chimeric polypeptide of the invention. It was
CC derived from a fusion of the human p27 and p16 cDNA sequences. The
CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
CC binding motifs from at least two different proteins that bind to CDKs.
CC The protein controls proliferation and/or differentiation of cells,
CC particularly they inhibit cell-cycle progression. They can be used to
CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
CC can also treat diseases associated with de-differentiation or
CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
CC diseases, gastric ulcers and autonomous diseases of the peripheral
CC nervous system. Other applications include reducing growth of hair and
CC protecting hair follicle cells against cytotoxic treatments, cosmetically
CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
CC oogenesis. The chimeric proteins can also be used in vitro to maintain
CC cells, especially neurons intended for testing specific activity of
CC trophic factors, at selected points in the cell cycle. The proteins are
CC more active inhibitors of the CDK/cyclin complex than binding motifs used
CC individually (since they may bind to CDK involved in different stages of
CC the cell cycle).
SQ Sequence 1098 BP; 234 A; 326 C; 378 G; 160 T;
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alignment\_scores:

Quality: 788.00 Length: 155  
Ratio: 5.117 Gaps: 0  
Percent Similarity: 99.355 Percent Identity: 99.355

alignment\_block:

US-09-016-869A-2 x T74053 ..

Align seg 1/1 to: T74053 from: 1 to: 1098

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18 rAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluAlaV 35
|||||
84 GCGCGCGCGCGGTCGGTAGAGAGTGGGCGCTGCTGGAGCGG 133

35 alAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51
|||||
134 GGGCGCTGCCCAACGACCGAATAGTACGTCGAGGCGCGATCCAGGTC 183
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52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAl 68  
|||||  
184 ATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTGCACGGCGC 233  
68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85  
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234 GGAGCCCAACTGGCGGACCCCGCACTCTCACCCGACCGGTGCACGACG 283  
85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101  
|||||  
284 CTGCCCCGGAGGGCTTCCTGGACACGCTGGTGGTGTGACCGGGCGGG 333  
102 AlaArgLeuAspValArgAspAlaTtpGlyArgLeuProValAspLeuAl 118  
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334 GCGGGCTGGACGTGCCGATGGCTGGGGCCGTCTGCCCTGGACCTGGC 383  
118 aGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaAlaG 135  
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384 TGAGGAGCTGGGCCATCGCGCATGTGCGACGGTACCTGCGCGGGCTGCGG 433  
135 lyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGlyPro 151  
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434 GGGGCACCAAGAGCAGTAACCATGCCCGCATAGATGCCCGGAAGGTCCC 483  
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484 TCAGACATCCCCGAT 498



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About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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; APPLICANT: Beach, David H.  
; APPLICANT: Serrano, Manuel A.  
; APPLICANT: Depinho, Ronald A.  
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
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; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
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; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 994 base pairs  
; TYPE: nucleic acid  
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; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
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34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50  
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117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
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; Sequence 1, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306.511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CF2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
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151 ProSerAspIleProAsp 156
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491 CCTCAGACATCCCGAT 508

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; Sequence 1, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
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; COUNTRY: USA
; ZIP: 02109
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; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEPTEMBER-1994
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; FILING DATE: 25-MAY-1994
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; FILING DATE: 14-APRIL-1994
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; FILING DATE: 18-NOVEMBER-1993
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; FILING DATE: 17-DECEMBER-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCTOBER-1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
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; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
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; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Elliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
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; FILING DATE: 02-JAN-1996
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; APPLICATION NUMBER: US 08/497,214
; FILING DATE: 30-JUN-1995
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; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
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; APPLICATION NUMBER: US 08/154,915
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; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
; LOCATION: 41..508
; US-08-581-918A-1

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; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
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; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
; LOCATION: 41..508
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51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
191 GTCATGATGGGCGGCGCTTCCTGGACACGCTGGTGGTGTGACCGG 240

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117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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151 ProSerAspIleProAsp 156
491 CCCTCAGACATCCCGAT 508
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; Patent No. 5624819

; GENERAL INFORMATION:

; APPLICANT: Skolnick, Mark H.

; APPLICANT: Cannon-Albright, Lisa A.

; APPLICANT: Kamb, Alexander

; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESSES:

; ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP

; STREET: 1201 New York Avenue, Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/474,177

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03537

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938

; FILING DATE: 01-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,087

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,086

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,369

; FILING DATE: 14-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/214,582

; FILING DATE: 18-MAR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Innen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24884-109348-E

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: Homo sapiens
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; GENERAL INFORMATION:

; APPLICANT: Kamb, Alexander

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; TITLE OF INVENTION: MTS1L-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
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; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: linear
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; HYPOTHEetical: NO
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- Patent No. 5801236
- GENERAL INFORMATION:
- APPLICANT: Kamb, Alexander
- TITLE OF INVENTION: MTS1 GENE
- NUMBER OF SEQUENCES: 36
- CORRESPONDENCE ADDRESS:
- ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
- STREET: 1201 New York Avenue, Suite 1000
- CITY: Washington
- STATE: DC
- COUNTRY: USA
- ZIP: 20005
- COMPUTER READABLE FORM:
- COMPUTER: IBM PC compatible
- OPERATING SYSTEM: PC-DOS/MS-DOS
- SOFTWARE: PatentIn Release #1.0, Version #1.30
- CURRENT APPLICATION DATA:
- APPLICATION NUMBER: US/08/480,810
- FILING DATE: 07-JUN-1995
- CLASSIFICATION: 435
- PRIOR APPLICATION DATA:
- APPLICATION NUMBER: PCT/US95/03316
- FILING DATE: 17-MAR-1995
- PRIOR APPLICATION DATA:
- APPLICATION NUMBER: US 08/251,938
- FILING DATE: 01-JUN-1994
- PRIOR APPLICATION DATA:
- APPLICATION NUMBER: US 08/215,087
- FILING DATE: 18-MAR-1994
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; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; CLASSIFICATION: 435
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; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
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; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Ramb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
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; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
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; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
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; ORGANISM: Homo sapiens
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; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
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; FILING DATE: 01-JUN-1994
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; FILING DATE: 18-MAR-1994
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; FILING DATE: 14-APR-1994
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; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
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; LENGTH: 471 base pairs
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; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
; US-09-115-252-1

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17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
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51 CACGGCGCGCGCGGGGTGGGTAGAGGAGTGGCGGCGTGGTGGAG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgProIleGln 50
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101 CGGGGGCGCTGCCAACGACCGCAATAGTTACGGTCGGAGCGCATCCAG 150
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl 67
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151 GTCATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 CGCGAGGCCCAACTCGCGCGGACCGCCGACCTCTACCCGACCCGTCGACG 250
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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251 ACGTCTCCCGGAGGCTTCTCTGGACACGCTGGTGTCTGCACCGGGCC 300
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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301 GGGGGCGGCTGGACGTGGCGATGCTGGGGCGGCTGCGCGTGGACCT 350
117 uAlaGluGluLeuGlyHisArgAspValAlaThrGlyLeuArgAlaAlaA 134
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351 GGCTGAGGAGCTGGCCATCGCATGTCGCACGCTACCTGCGCGGCGCTG 400
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleaspAlaAlaGluGly 150
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401 CGGGGGCACCGAGGAGTAAACCATGCCCGCATAGATGCCCGGGAAGT 450
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451 CCCTCAGACATCCCGAT 468

seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-474-177-36
seq_documentation_block:
; Sequence 36, Application US/08474177
; Patent No 5624819
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: /note= "Splice site acceptor."
;
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; US-08-474-177-36

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    Percent Similarity: 99.359    Percent Identity: 98.718

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|||||
34 IaValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
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|||||
51 ValMetMetMetGlySerAlaAlaArgValAlaGluLeuLeuLeuHisGl 67
|||||
151 GTCATGATGATGGCAGCGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||
201 CGCGAGGCCCACTCGCGGACCCCGCCACTCTCACCGACCGGTGCACG 250
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84 sAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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|||||
351 GGCTGAGGAGCTGGGCCATCGCGATGTGCGACGTACCTGCGCGGGCTG 400
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134 IaGlyGlyThrArgGlySerAsnHisAlaAArgIleAspAlaAlaGluGly 150
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451 CCTCAGACATCCCGAT 468

seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-487-033-36

seq_documentation_block:
; Sequence 36, Application US/08487033
; Patent No. 5735027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
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Align seg 1/1 to: US-08-487-033-36 from: 1 to: 947

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51 CACGGCCCGCCCGGGTTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100  
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201 CGGGAGCCCAACTGGCGCGACCCCGCCACTCTCACCCGACCCGTGCACG 250  
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451 CCCTCAGACATCCCGGAT 468





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77 hrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThr 93
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94 LeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTr 110
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416 CTGCGGTGTCTACCGCGCGGGCGCGGTGGACGTGCGCGATGCTG 367
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110 pClyArgLeuProValAspLeuAlaGluLeuGlyHisArgAspValA 127
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366 GGGCGGTGTGCCCGTGGACCTGGCTGGAGAGCTGGGCCATCGCATG 317
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127 laArgTyrLeuArgAlaAlaAlaGlyGlyThrArgGlySerAsnHisAla 143
|||||
316 CACGTACTTGGCGCGGTGCGGGGGGCCAGCAGAGCAGTAACCATGCC 267
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similar to TR:016361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION AI871381
VERSION AI871381.1 GI:5545430
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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strand cDNA was primed with a Not I - Oligo(dT) primer [5'
TGTACCAATCTCAAGTGGGAGCGCGCATAGTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI

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adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

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ORIGIN

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|||||
83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
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100 AlaGlyAlaArgLeuAspValArgAspAlaTrpClyArgLeuProValA 116
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116 pLeuAlaGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAla 133
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366 CTTGCTGAGGAGCTGGCGCATCCGATGTGCGACGATCTGTCGCCG 317
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133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
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316 CTGCGGGGGGCCAGCAGAGGAGTAACCATGCCCATAGATGCCCGGAA 267
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ACCESSION AW328496
VERSION AW328496.1 GI:6798992
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 648)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036295.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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www-bio.llnl.gov/bbrp/image/image.html
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  Percent Similarity: 100.000      Percent Identity: 100.000
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83 iAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
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209 ACGAGCTGCCCGGAGGCTTCCTGGACAGCTGGTGGTCTGCACCGG 258
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValH 116
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116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
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309 CCTGGCTGAGGAGTGGGCCATCGGATGTCGACGCTACCTGCGCGGG 358
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
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;; mRNA sequence.
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VERSION        AI870879.1 GI:5544847
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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  National Cancer Institute / National Institute of Neurological
  Disorders and Stroke, Brain Tumor Genome Anatomy Project
  (CGAP/DTGAP), Tumor Gene Index
  Unpublished (1998)
  On May 18, 1998 this sequence version replaced gi:3136859.
  Contact: Robert Strausberg, Ph.D.
  Email: Robert.Strausberg@nih.gov
  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
  Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
  Bonaldo, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
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      TGTACCATCTGAAGTGGAGCGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
      T 3']; double-stranded cDNA was ligated to Eco RI
      adaptors (Pharmacia), digested with Not I and cloned into
      the Not I and Eco RI sites of the modified pT7T3 vector.
      Library is normalized, and was constructed by Bento
      Soares and M. Fatima Bonaldo."
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66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
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83 iAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
|||||
455 ACGAGCTGCCCGGAGGCTTCCTGGACAGCTGGTGGTCTGCACCGG 406
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValH 116
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116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 580)  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
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 Seq primer: -40UP from Gibco  
 High quality sequence stop: 321.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2014405"  
 /clone\_lib="NCI\_CGAP\_Brn25"  
 /tissue\_type="glioblastoma (pooled)"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCCGATATCTTTTITTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 116 a 160 c 174 g 130 t  
 ORIGIN

## FEATURES

source  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2014405"  
 /clone\_lib="NCI\_CGAP\_Brn25"  
 /tissue\_type="glioblastoma (pooled)"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCCGATATCTTTTITTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

alignment\_scores:  
 Quality: 532.00 Length: 107  
 Ratio: 5.067 Gaps: 0  
 Percent Similarity: 98.131 Percent Identity: 97.196

## alignment\_block:

US-09-016-869a-2 x AI362049/rev ..

Align seg 1/1 to reverse of: AI362049 from: 1 to: 580

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 66  
 |||  
 556 CAGGTGCATGATGGCGAGCGCTCGAGTGGCGGAGCTGCTGCTCCA 507  
 |||  
 66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83  
 |||  
 506 CGCGCGGAGCCCACTCGCGGACTCGCCACTCTCACCGAACCGTGC 457  
 |||  
 83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99  
 |||  
 456 ACAGACGCTGCCCGGAGGCTCTCTGAACACGCTGGTGTGTCACCGG 407  
 |||  
 100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116  
 |||  
 406 GC CGCGGCGCGCTGCGACGTGCGCGATGCTGGGCGCTGCTGCCGTGA 357  
 |||  
 116 pleuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133  
 |||  
 356 CTGTGCTGAGGAGCTGGGCCATCGCGATGTCGACGGTACCTGCGCGG 307  
 |||  
 133 laAlaGlyClyThrArgGlySerAsnHisAlaArgIleAspAlaGlu 149  
 |||  
 306 CTGCGGGGGGACACAGAGCAGTACCATGCCGATAGATGCCGGGAA 257  
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 150 GlyProSerAspIleProasp 156  
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 256 GGTCCCTCAGACATCCCGAT 236  
 seq\_name: gb\_est17:AI198233

## seq\_documentation\_block:

LOCUS AI198233 579 bp mRNA EST 02-DEC-1998  
 DEFINITION Q155d12.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3', similar to TR:Q16361.Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM mRNA sequence.  
 contains LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI198233  
 VERSION AI198233.1 GI:3750839  
 KEYWORDS EST.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 579)  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
 Unpublished (1998)

## JOURNAL

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D. Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 729 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 459.

Location/Qualifiers

## FEATURES

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/lab\_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCCGACATAGGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 158 c 177 g 130 t 1 others  
ORIGIN

alignment\_scores:  
Quality: 531.00 Length: 107  
Ratio: 5.009 Gaps: 0  
Percent Similarity: 99.065 Percent Identity: 96.262

alignment\_block:  
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|||||  
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83  
|||||  
505 CAGCGCGAAGCCCAACTGCGCGAGCGCCACTCTCACCGACCCGCTGC 456  
|||||  
83 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99  
|||||  
455 ACACGCTGCGCGGAGGGCTTCGTGACACGCTGGTGGTGTGCACCG 406  
|||||  
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116  
|||||  
405 GCGGGGCGCGGCTGGACGTGGCGATGCTGGGGCCGCTGCGCGGTGGA 356  
|||||  
116 pLeuAlaGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAla 133  
|||||  
355 CTTGGCTGAGGAGCTGGCCATCGCATGTCGCACGCTACCTGCGCGCG 306  
|||||  
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149  
|||||  
305 CTGCGGGGCGCACAGAGGAGTAAACCATGCCCGCATAGATGCCGCGGAA 256  
|||||  
150 GlyProSerAspIleProAsp 156  
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255 GTTCCCTCAGACATCCCCGAT 235

seq\_name: gb\_est25:A1765096

seq\_documentation\_block:  
LOCUS A1765096 774 bp mRNA EST 21-DEC-1999  
DEFINITION w148b08.x1 NCI\_CGAP\_Col6 Homo sapiens cDNA clone IMAGE:2393463 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains LTR3.b3 MER22 repetitive element ; , mRNA sequence.  
ACCESSION A1765096  
VERSION A1765096.1 GI:5231605  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 774)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Feb 22, 1999 this sequence version replaced gi:4283180.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
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Seq primer: -40UP from Gibco  
High quality sequence stop: 400.

#### FEATURES

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/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 153 a 220 c 221 g 179 t 1 others  
ORIGIN

#### alignment\_scores:

Quality: 529.00 Length: 158  
Ratio: 4.336 Gaps: 2  
Percent Similarity: 77.215 Percent Identity: 69.620

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US-09-016-869A-2 x A1765096/rev ..  
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713 TGGTTTCATCCCGCGGCTCACGGGGAGG..... 684  
31 uLeuGluAlaValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgp 48  
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683 .....TGGGCACGCCGAGGGCGGCCCGCGCTGTGGGCATCGTG 644  
48 rolle..... 49  
643 CTTATGCTATTAGGAGCCCGAGCGTTTAGGCACGACCGCTTCCTAGAA 594  
50 ...GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLe 65  
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593 GACCAGGTCTATGATGATGGCAGCGCCGCGAGTGGCGGAGCTGCTGCT 544  
65 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProv 82  
|||||  
543 CCACGGCGCGAGCCCAATTGGCGCGACCCGCCCACTTCCACCCGACCG 494  
82 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 98  
|||||  
493 TGCACGACGCTGCCCGAGGGCTTCTTGACACGCTGGTGGTGTGCAC 444  
99 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 115  
|||||  
443 CGGGCCCGCGGGCTGGACGTGGCAATGCTGGGGCGCGCTGCCCCGT 394  
115 lAspLeuAlaGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArg 132  
|||||





cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cdna Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html  
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High quality sequence stop: 394.  
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/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TTTACCAATCGAAGTGGCGCCGATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 137 a 210 c 219 g 140 t 2 others  
ORIGIN

alignment\_scores:  
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Ratio: 5.019 Gaps: 0  
Percent Similarity: 97.196 Percent Identity: 95.327  
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US-09-016-869A-2 x AI363262/rev ..  
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540 CAGGTCATGATGATGGCAAGCGCCGAGTGGGAGCTGCTGCTCCC 491  
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83  
|||||  
490 GGGCGCGAGCCCAACTCGCAGCAGCCGCCCAACTCTCACCAGCCCGTGC 441  
83 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99  
|||||  
440 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGTGTCGACCGG 391  
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116  
|||||  
390 GCCGGGGCGCGCTGAGCTGGCGCATGCCCTGGGGCCGCTCTGCCCGTGA 341  
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133  
|||||  
340 CCTGGCTGAGGAGCTGGCCCATCGGATGTCGACGGTACCTGCGCGCG 291  
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaGlu 149  
|||||  
290 CTGCGGGGGGACCAAGAGCAGTAACCATGCCCCGATAGATGTCGCCGAA 241  
150 GlyProSerAspIleProAsp 156  
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240 GGTCCCTCAGACATCCCCGAT 220

seq\_name: gb\_est27:AI954684

seq\_documentation\_block:  
LOCUS AI954684 563 bp mRNA EST 08-MAR-2000

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

wq34hl2 x1 NCI-CGAP\_GC6 Homo sapiens cdna clone IMAGE:2473223 3'  
similar to SW:CDN2\_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR  
A ; mRNA sequence.  
AI954684  
AI954684.1 GI:5746994  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 563)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
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/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
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NCI-CGAP\_GC4 was prepared, and as circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (cloneids 1257096-1258631,  
1469064-1470983, and 1475592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldo."  
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ORIGIN

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Percent Similarity: 95.495 Percent Identity: 94.595  
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563 AGGCAAAATGTAGGGGTCATGATGGGAGCGCCCGAGTGGCGGAGCT 514  
62 uLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThrLeu 79  
|||||  
513 CTGCTGCTCCACGGCGGGAGCCCACTG.CCGACCCCGCACTCTCA 465  
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NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clones 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaudo.
BASE COUNT      107 a  144 c  163 g      116 t      1 others
ORIGIN

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  Percent Similarity: 98.990      Percent Identity: 98.990

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531 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGGCCCACTGCGCGA 482
74 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 91
481 CNCCGCCACTCTCACCGACCCGTGCACGAGCTGCCGGGAGGGCTTCC 432
91 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 107
431 TGGACACGCTGGTGTGCTGCACCGGCGCGCGCTGCAGCTGCGC 382
108 AspAlaTrpGlyArgLeuProValAspLeuAlaGluLeuGlyHisAr 124
381 GATCCCTGGGGCGCTGCTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 332
124 gAspValAlaArgTyrLeuArgAlaAlaGlyGlyThrArgGlySerA 141
331 CGATGTGCACGATACCTGCGCGGGCTGCCGGGGACACAGAGGCAGTA 282
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                  ;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION      AI638416
VERSION        AI638416.1 GI:4690650
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 528)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        On Apr 7, 1998 this sequence version replaced gi:3036438.
              Contact: Robert Strausberg, Ph.D.
              Tel: (301) 496-1550
              Email: Robert_Strausberg@nih.gov
              Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
```

```
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaudo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 648 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.

FEATURES
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    /lab_host="DH10B"
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    NCI_CGAP_GC4 was prepared, and ss circles were made in
    vitro. Following HAP purification, this DNA was used as
    tracer in a subtractive hybridization reaction. The driver
    was PCR-amplified cDNAs from a pool of 5,000 clones made
    from the same library (clones 1257096-1258631,
    1469064-1470983, and 1475592-1476743). Subtraction by
    Bento Soares and M. Fatima Bonaudo.
    BASE COUNT      106 a  143 c  163 g      114 t      2 others
    ORIGIN

alignment_scores:
  Quality: 502.00      Length: 99
  Ratio: 5.122        Gaps: 0
  Percent Similarity: 98.990      Percent Identity: 97.980

alignment_block:
US-09-016-869A-2 x AI638416/rev ..
Align seg 1/1 to reverse of: AI638416 from: 1 to: 528

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528 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGGCCCACTGCGNGA 479
74 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 91
478 CNCCGCCACTCTCACCGACCCGTGCACGAGCTGCCGGGAGGGCTTCC 429
91 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 107
428 TGGACACGCTGGTGTGCTGCACCGGCGCGGCTGCAGCTGCGC 379
108 AspAlaTrpGlyArgLeuProValAspLeuAlaGluLeuGlyHisAr 124
378 GATCCCTGGGGCGCTGCTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 329
124 gAspValAlaArgTyrLeuArgAlaAlaGlyGlyThrArgGlySerA 141
328 CGATGTGCACGATACCTGCGCGGCTGCCGGGGACACAGAGGCAGTA 279
141 snHisAlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
278 ACCATGCCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGCAT 232

seq_name: gb_est36:AW006218

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DEFINITION      wz93g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566424 3'
                  similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
                  ;, mRNA sequence.
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VERSION        AW006218.1
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SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 579)
AUTHORS        NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute / National Institute of Neurological
               Disorders and Stroke, Brain Tumor Genome Anatomy Project
               (CGAP/BTGNP), Tumor Gene Index
JOURNAL        Unpublished (1998)
COMMENT        On Oct 6, 1998 this sequence version replaced gi:3705694.
               Contact: Robert Strausberg, Ph.D.
               Tel: (301) 496-1550
               Email: Robert.Strausberg@nih.gov
               Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
               Ph.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
               Bonaldo, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Seq primer: -40UP from Gibco
               High quality sequence stop: 461.

FEATURES       1. 579
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               /db_xref="taxon:9606"
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               /clone_lib="NCI-CGAP_Brn25"
               /tissue_type="anaplastic oligodendroglioma"
               /lab_host="DH10B"
               /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
               modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
               strand cDNA was primed with a Not I - oligo(dT) primer [5'
               TGTTACCAATCTGAAGTGGAGCGCGCATAGTTTGTGTTTTTTTTTTTTTTT
               T 3']; double-stranded cDNA was ligated to Eco RI
               adaptors (Pharmacia), digested with Not I and cloned into
               the Not I and Eco RI sites of the modified pT73 vector.
               Library is normalized, and was constructed by Bento
               Soares and M. Fatima Bonaldo."
BASE COUNT     113 a 161 c 172 g 131 t
ORIGIN

alignment_scores:
  Quality: 484.00      Length: 107
  Ratio: 4.654         Gaps: 0
  Percent Similarity: 97.196 Percent Identity: 95.327

alignment_block:
  US-09-016-869A-2 x AW006218/rev ..

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554  AAGGTGATGATGATGAGAGCGCCGAGG.GCGGAGCTGCTGCTGCTCCA 506
    |||:|||||
66  sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
    |||:|||||
505  CGGGNGGAGCCCAANTGCGGGACCGCC.ACTCTCACCCGACCGCTGC 457
    |||:|||||
83  isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
    |||:|||||
456  ACGACGCTGCCGGAGGGCTTCTCGACACGCTGCTGCTGCACCGG 407
    |||:|||||
100  AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
    |||:|||||
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406  GCCGGGGCGCGCTGGACGTGGCGGATCCCTGGGGCCCTCTGCGCGTGA 357
116  pleuAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
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356  CCGTGCCTGAGGAGCTGGCCATCGCGATGTCGACGGTACCTGCGCGCG 307
133  laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
    |||:|||||
306  CTGCGGGGGGACCAGAGCAGTACCATGCCGCGCATAGATGCCGCGGAA 257
150  GlyProSerAspIleProAsp 156
    |||:|||||
256  GGTCCCTCAGACATCCCGAT 236
seq_name: gb_est9:AA557137

seq_documentation_block:
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  DEFINITION n174505.s1 NCI-CGAP_Br2 Homo sapiens cDNA clone IMAGE:1056369 3',
  similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
  A ; mRNA sequence.
  ACCESSION   AA557137
  VERSION     AA557137.1 GI:2327614
  KEYWORDS    EST.
  SOURCE      human.
  ORGANISM    Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE   1 (bases 1 to 599)
  AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
  JOURNAL     Unpublished (1997)
  COMMENT     On Jan 14, 1998 this sequence version replaced gi:1877968.
               Contact: Robert Strausberg, Ph.D.
               Tel: (301) 496-1550
               Email: Robert.Strausberg@nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Insert Length: 755 Std Error: 0.00
               Seq primer: -40ml3 fwd. Et from Amersham
               High quality sequence stop: 410.

FEATURES       1. 599
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               /clone_lib="NCI-CGAP_Br2"
               /sex="female, pooled"
               /tissue_type="breast"
               /lab_host="DH10B"
               /note="Vector: pT73D-Pac (Pharmacia) with a modified
               polylinker; 1st strand cDNA was prepared from pooled bulk
               breast tumor tissue, and was then primed with a Not I -
               oligo(dT) primer. Double-stranded cDNA was ligated to Eco
               RI adaptors (Pharmacia), digested with Not I and cloned
               into the Not I and Eco RI sites of the modified pT73
               vector. This library is the normalized version of
               NCI CGAP_Brl.1. Library was constructed by Bento Soares
               and M. Fatima Bonaldo."
BASE COUNT     123 a 163 c 179 g 134 t
ORIGIN

alignment_scores:
  Quality: 484.00      Length: 119
  Ratio: 4.209         Gaps: 1
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Percent Similarity: 96.639   Percent Identity: 88.235
alignment_block:
US-09-016-869A-2 x AA557137/rev  ..

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55  ySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnC 72
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
537 CCAGCCCCGAATGCGGAATCTGCTGCTCCACGC.GCGGAGCCCAAT 489

72  ysAlaAspProAlaThrLeuThrArgProValHisAspAlaAlaArgGlu 88
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
488 GCGCCGACCCGCCAATCTCACCAGACCCGTCGACGAGCGCTGCCCGGAG 439

89  GlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAs 105
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
438 GGCTTCTTGACACGCTGGTGGTCTGCACCGCGCGGGCGGCGCTGGA 389

105 pValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGluLeuG 122
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
388 CGTGCGCGATGCCCTGGGC.CGTCTGCCCTGGACCTGGCTGAGGAGCTGG 340

122 lyHisArgAspValAlaArgTyr.LeuArgAlaAlaAlaGlyGlyThr 138
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
339 GCCATTGCGATGTCGCACGGTACTCTGCGCGCGGCTGCGGGGGCACAG 290

138 gGlySerAsnHisAlaArgIleAspAlaAlaGluGlyProSerAspIle 155
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
289 AGCAGTAAACCATGCCCGCATAGATCCCGGGAAGGTCCCTCAGACATCC 240

155 roAsp 156
   ::::
239 CCGAT 235

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:04:57 ; Search time 2513.97 Seconds  
(without alignments)  
594.196 Million cell updates/sec

Title: US-09-016-869A-3  
Perfect score: 837  
Sequence: 1 GAGGACTCCGCGACGGTCCG.....AGGCTGCCAACGGGAGCGG 837

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues 1945680  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_om: \*  
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5: gb\_pat: \*  
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8: gb\_pl2: \*  
9: gb\_pr1: \*  
10: gb\_pr2: \*  
11: gb\_pr3: \*  
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24: em\_ph: \*  
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28: em\_sy: \*  
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47: em\_htg3: \*  
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53: gb\_htg10: \*  
54: gb\_htg11: \*  
55: gb\_htg12: \*  
56: gb\_htg13: \*  
57: gb\_htg14: \*  
58: gb\_in3: \*  
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60: gb\_htg16: \*  
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63: em\_htg5: \*  
64: em\_htg6: \*  
65: em\_htg7: \*  
66: em\_hum6: \*  
67: gb\_htg18: \*  
68: gb\_htg19: \*  
69: gb\_htg20: \*  
70: gb\_htg21: \*  
71: gb\_htg22: \*  
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76: gb\_htg27: \*  
77: gb\_htg28: \*  
78: gb\_htg29: \*  
79: gb\_htg30: \*  
80: gb\_htg31: \*  
81: gb\_v11: \*  
82: gb\_v12: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	837	100.0	837	9	HUMCIP	L36844 Homo sapien
2	677.2	80.9	751	5	AR001326	AR001326 Sequence
3	677.2	80.9	751	5	AR037506	AR037506 Sequence
4	677.2	80.9	751	5	AR062786	AR062786 Sequence
5	677.2	80.9	751	5	I41160	I41160 Sequence 15
6	672	80.3	738	11	HSU17075	U17075 Human p14-C
7	540.2	64.5	859	11	AF004819	AF004819 Homo sapi
8	418.2	50.0	753	39	S75756	S75756 p15-cyclin
9	418.2	50.0	44160	39	AC000049	AC000049 Homo sapi
10	360	43.0	457	39	S69805	S69805 MTS2-multip
11	360	43.0	1244	5	AR001317	AR001317 Sequence
12	360	43.0	1244	5	AR037497	AR037497 Sequence
13	360	43.0	1244	5	AR062777	AR062777 Sequence
14	360	43.0	1244	5	I41151	I41151 Sequence 5
15	330.4	39.5	2147	39	AF058758	AF058758 Homo sapi
16	278.4	33.3	1301	12	AF059567	AF059567 Mus muscu
17	277	33.1	706	12	S79760	S79760 Ink4 I rats,
18	266.8	31.9	471	5	AR001314	AR001314 Sequence
19	266.8	31.9	471	5	AR037494	AR037494 Sequence
20	266.8	31.9	471	5	AR062774	AR062774 Sequence
21	266.8	31.9	471	5	I41148	I41148 Sequence 1
22	266.8	31.9	947	5	AR001346	AR001346 Sequence
23	266.8	31.9	947	5	AR037526	AR037526 Sequence
24	266.8	31.9	947	5	AR062806	AR062806 Sequence

25 266.8 31.9 947 5 I41180  
26 266.8 31.9 987 10 HOMINK4X  
27 265.6 31.7 1420 5 I67718  
28 265.4 31.7 393 5 AR062815  
29 251.4 30.0 742 20 AB010808  
30 232 27.7 660 11 S78535  
31 232 27.7 1017 10 HSU26727  
32 232 27.7 1131 5 AR001325  
33 232 27.7 1131 5 AR037505  
34 232 27.7 1131 5 AR062785  
35 232 27.7 1131 5 I41159  
36 230.6 27.6 457 39 S69804  
37 230.6 27.6 540 39 S69822S1  
38 230.6 27.6 585 11 HSPCDK2  
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## ALIGNMENTS

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LOCUS Homo sapiens (clone p15INK4B/HA5) CDK inhibitory protein mRNA,  
DEFINITION complete cds.  
ACCESSION L36844  
VERSION L36844.1 GI:556197  
KEYWORDS CDK inhibitory protein.  
SOURCE Homo sapiens cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 837)  
AUTHORS Hannon.G.J. and Beach.D.  
TITLE p15INK4B is a potential effector of TGF-beta induced cell cycle  
arrest  
JOURNAL Nature 371, 257-261 (1994)  
MEDLINE 94359613  
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ORIGIN  
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Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGACTCCGCGACGGTCCGCGACCTGCGCGCAGAGCGGCTTTGAGCTCGGCTGCTCCG 60  
DB 1 GAGGACTCCGCGACGGTCCGCGACCTGCGCGCAGAGCGGCTTTGAGCTCGGCTGCTCCG 60

QY 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCCCGCTGTGTTCTTTGAGCGCCAGGA 120  
DB 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCCCGCTGTGTTCTTTGAGCGCCAGGA 120  
QY 121 AAAGCCCGGAGCTACGACCGCGCGCTCGGCACTGCACGGGGCCCCCAAGCGCGCAAGAA 180  
DB 121 AAAGCCCGGAGCTACGACCGCGCGCTCGGCACTGCACGGGGCCCCCAAGCGCGCAAGAA 180  
QY 181 GGACGACGGGAGGTAATGAAGCTGAGCCAGTCTCTCTAGGAAGGAGAGTAGTGGCGCGG 240  
DB 181 GGACGACGGGAGGTAATGAAGCTGAGCCAGTCTCTCTAGGAAGGAGAGTAGTGGCGCGG 240  
QY 241 AGCAGCGTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCCAACGCTGATATATCCG 300  
DB 241 AGCAGCGTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCCAACGCTGATATATCCG 300  
QY 301 GGCGCTCGCGCTGTGGGGCTGCGGAATGCGGAGGAGAACAGGGCATGCCAGTGGG 360  
DB 301 GGCGCTCGCGCTGTGGGGCTGCGGAATGCGGAGGAGAACAGGGCATGCCAGTGGG 360  
QY 361 GGCGCAGCGATGAGGGTCTGGCCACGCGCGGGGACTAGTGGAAGGTGCGACAC 420  
DB 361 GGCGCAGCGATGAGGGTCTGGCCACGCGCGGGGACTAGTGGAAGGTGCGACAC 420  
QY 421 TCCTGGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGCGCGCGATCCAG 480  
DB 421 TCCTGGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGCGCGCGATCCAG 480  
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DB 481 GTCATGATGAGGCGCGCGCGCGCGTGGCGGAGTGTGCTGCTCCAGCGCGCGAGGCC 540  
QY 541 AACTGCGCAGACCTTCCACCTCTCACCGACCGGTGTCATGATGCTGCCCGGAGGGCTTC 600  
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QY 661 GGTGCTGTGCGCGTGGACTTGGCGAGGAGCGGGCCACCGGAGTGTGCGGATGCTCTGG 720  
DB 661 GGTGCTGTGCGCGTGGACTTGGCGAGGAGCGGGCCACCGGAGTGTGCGGATGCTCTGG 720  
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DB 721 CGCAGCAGCGGCGGACTGACCGCAGGTTCGCCAGCGCGCCCAACACGACTTTATTTCT 780  
QY 781 TACCCAAATTTCCACCCCG 837  
DB 781 TACCCAAATTTCCACCCCG 837

## RESULT 2

AR001326 751 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 15 from patent US 5739027.  
ACCESSION AR001326  
VERSION AR001326.1 GI:3963393  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 751)  
AUTHORS Kamb,A.  
TITLE MTS1E1.beta. gene  
JOURNAL Patent: US 5739027-A 15 14-APR-1998;  
FEATURES Location/Qualifiers  
source 1..751  
BASE COUNT 130 a 225 c 292 g 104 t  
ORIGIN



FEATURES		Location/Qualifiers	
source		1..751	
BASE COUNT		130 a 225 c 292 g 104 t	
ORIGIN			
Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
DB	186	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	245
QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
DB	246	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	305
QY	299	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
DB	306	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
DB	366	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
DB	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCCACGGCGCGG	535
DB	486	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCTCACGGCGCGG	545
QY	536	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
DB	546	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	655
DB	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	715
DB	666	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	725
QY	716	ACCTGCGCACAGCCACGGGGGACTGA 741	
DB	726	ACCTGCGCACAGCCACGGGGGACTGA 751	
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AR062786			
LOCUS	AR062786	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5843756.		
ACCESSION	AR062786		
VERSION	AR062786.1 GI:5990477		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
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QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
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QY	299	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
DB	306	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
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QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
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QY	476	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCCACGGCGCGG	535
DB	486	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCTCACGGCGCGG	545
QY	536	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
DB	546	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	655
DB	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	715
DB	666	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	725
QY	716	ACCTGCGCACAGCCACGGGGGACTGA 741	
DB	726	ACCTGCGCACAGCCACGGGGGACTGA 751	
RESULT 3			
AR037506			
LOCUS	AR037506	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5801236.		
ACCESSION	AR037506		
VERSION	AR037506.1 GI:5955362		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
DB	186	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	245
QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
DB	246	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	305
QY	299	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
DB	306	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
DB	366	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
DB	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCCACGGCGCGG	535
DB	486	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCTCACGGCGCGG	545
QY	536	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
DB	546	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	655
DB	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	715
DB	666	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	725
QY	716	ACCTGCGCACAGCCACGGGGGACTGA 741	
DB	726	ACCTGCGCACAGCCACGGGGGACTGA 751	
RESULT 3			
AR037506			
LOCUS	AR037506	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5801236.		
ACCESSION	AR037506		
VERSION	AR037506.1 GI:5955362		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
DB	186	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	245
QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
DB	246	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	305
QY	299	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
DB	306	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
DB	366	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
DB	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCCACGGCGCGG	535
DB	486	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCTCACGGCGCGG	545
QY	536	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
DB	546	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	655
DB	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	715
DB	666	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	725
QY	716	ACCTGCGCACAGCCACGGGGGACTGA 741	
DB	726	ACCTGCGCACAGCCACGGGGGACTGA 751	
RESULT 3			
AR037506			
LOCUS	AR037506	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5801236.		
ACCESSION	AR037506		
VERSION	AR037506.1 GI:5955362		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
DB	186	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	245
QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
DB	246	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	305
QY	299	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
DB	306	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
DB	366	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
DB	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCCACGGCGCGG	535
DB	486	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCTCACGGCGCGG	545
QY	536	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
DB	546	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	655
DB	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	715
DB	666	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	725
QY	716	ACCTGCGCACAGCCACGGGGGACTGA 741	
DB	726	ACCTGCGCACAGCCACGGGGGACTGA 751	
RESULT 3			
AR037506			
LOCUS	AR037506	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5801236.		
ACCESSION	AR037506		
VERSION	AR037506.1 GI:5955362		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
DB	186	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	245
QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
DB	246	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	305
QY	299	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
DB	306	CGGCGCGCTGCGGCTCTGGGGGCTCGGAAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
DB	366	GGGCGCGCAGCATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
DB	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCCACGGCGCGG	535
DB	486	TCAGTCTCATGATGATGGGAGCGCGCGGCTGGCGAGTGTCTGCTCTCACGGCGCGG	545
QY	536	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
DB	546	AGCCCAACTGCGCAGACCTGCGCACTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	655
DB	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGCGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	715
DB	666	CCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGACGTTGCAGGGT	725
QY	716	ACCTGCGCACAGCCACGGGGGACTGA 741	
DB	726	ACCTGCGCACAGCCACGGGGGACTGA 751	
RESULT 3			
AR037506			
LOCUS	AR037506	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5801236.		
ACCESSION	AR037506		
VERSION	AR037506.1 GI:5955362		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
DB	9	GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	68
QY	60	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
DB	69	GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACAGCCGCGCTCGG-CACCTGACAGGCGGCCCAAGCCGCAAG	178
DB	129	AAAGCCCGGAGCTAACAGCCGCGCTCGGCACTGACAGGCGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	238
DB	186	AAGGACGCGGAGGCTAATGAGCTGAGCCAGCTCTCTAGGAAGGAGAGTGGCC	245
QY	239	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
DB	246	GGAGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAAC	

MTS1 genes  
encoding mutant MTS1 genes  
Patent: US 5801236-A 15 01-SEP-1998;



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RESULT 6
HSU17075      738 bp  mRNA      PRI
DEFINITION   Human p14-CDK inhibitor mRNA, complete cds.
ACCESSION   U17075
VERSION     U17075.1 GI:639715
KEYWORDS    human.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 738)
AUTHORS    Guan,K.L., Jenkins,C.W., Li,Y., Nichols,M.A., Wu,X., O'Keefe,C.L.,
            Matera,A.G. and Xiong,Y.
TITLE      Growth suppression by p18, a p16INK4/MTS1- and
            p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb
            function.
JOURNAL    Genes Dev. 8 (24), 2939-2952 (1994)
MEDLINE   95095079
REFERENCE   2 (bases 1 to 738)
AUTHORS    Guan,K.
TITLE      Direct Submission
JOURNAL    Submitted (09-NOV-1994) Kun-Liang Guan, Biological Chemistry,
            University of Michigan, 1301 East Catherine, Ann Arbor, MI 48109,
            USA
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Best Local Similarity 97.8%; Pred. No. 5.5e-102;
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QY 195 TAATGAAGCTGAGCCAGCTCTCTAGGAAGGAGAGAGTGCGCCGAGCAGCGTGGGAAA 254
Db 189 TAATGAAGCTGAGCCAGCTCTCTAGGAAGGAGAGAGTGCGCCGAGCAGCGTGGGAAA 248
QY 255 GAAGGGAAGAGTCTCCTTAAGTTTACGGCAACCGGTGGATTATCCGGGCGCTGCGCGTC 314
Db 249 GAAGGGAAGAGTCTCCTTAAGTTTACGGCAACCGGTGGATTATCCGGGCGCTGCGCGTC 308
QY 315 TGGGGGCTGCGGAATCGCGGAGAGAACAGAGCGCATGCCAGTGGGGCGGCGACGCGATGA 374
Db 309 TGGGGGCTGCGGAATCGCGGAGGAGAACAGAGCGCATGCCAGTGGGGCGGCGACGCGATGA 368
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QY 672 CGTGACTTGGCCGAGGAGCGGGGCCACCGCACGTTTGCAGGTACCTGCGCACAGCCAC 731
Db 669 CGTGACTTGGCCGAGGAGCGGGGCCACCGCACGTTTGCAGGTACCTGCGCACAGCCAC 728
QY 732 GGGGGACTGA 741
Db 729 GGGGGACTGA 738
RESULT 7
AF004819      859 bp  mRNA      PRI
DEFINITION   Homo sapiens alternative spliced form of p15 CDK inhibitor mRNA,
            complete cds.
ACCESSION   AF004819
VERSION     AF004819.1 GI:2257934
KEYWORDS    human.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 859)
AUTHORS    Tsubari,M., Tihoonen,E. and Laiho,M.
TITLE      Cloning and characterization of p10, an alternatively spliced form
            of p15 cyclin-dependent kinase inhibitor
JOURNAL    Cancer Res. 57 (14), 2966-2973 (1997)
MEDLINE   97373727
REFERENCE   2 (bases 1 to 859)
AUTHORS    Tsubari,M., Tihoonen,E. and Laiho,M.
TITLE      Direct Submission
JOURNAL    Submitted (20-MAY-1997) Department of Virology, Haartman Institute,
            University of Helsinki, P.O. Box 21, Helsinki 00014, Finland.
FEATURES   Location/Qualifiers
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                        /db_xref="GI:2257935"
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BASE COUNT 144 a 257 c 338 g 120 t
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Query Match 64.5%; Score 540.2; DB 11; Length 859;
Best Local Similarity 83.8%; Pred. No. 2.9e-80;
Matches 715; Conservative 0; Mismatches 8; Indels 130; Gaps 4;
QY 16 GTCCGCACCTCGCGCCAGAGCGGCTTTTCAGCTCGGCTGCTCCGCGCTAGGCGCTTTT 75
Db 10 GTCCGCACCTCGCGCCAGAGCGGCTTTTCAGCTCGGCTGCTCCGCGCTAGGCGCTTTT 69
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QY 718 CTGGCAGACAGCCAGGGGAGCTGAGCCAGGTTCCACAGCCGCCACACAGACTTTATTT 777  
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QY 778 TCTTACCAATTTCCACACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837  
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Db 398 TCTTACCAATTTCCACACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 457  
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RESULT 11  
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DEFINITION Sequence 5 from patent US 5739027.  
ACCESSION AR001317  
VERSION AR001317.1 GI:3963384  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1244)  
AUTHORS Kamb,A.  
TITLE MTS1L beta. gene  
JOURNAL Patent: US 5739027-A 5 14-APR-1998;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 571 TCTTACCAATTTCCACACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 630  
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RESULT 12  
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DEFINITION Sequence 5 from patent US 5801236.  
ACCESSION AR037497  
VERSION AR037497.1 GI:5955353  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1244)  
AUTHORS Kamb,A.  
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes

JOURNAL Patent: US 5801236-A 5 01-SEP-1998;  
FEATURES Location/Qualifiers  
source 1..1244  
/organism="unknown"  
BASE COUNT 279 a 343 c 355 g 260 t 7 others  
ORIGIN

Query Match 43.0%; Score 360; DB 5; Length 1244;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTCATGATGGGAGCGCCGCGTGGCGGAGCTGCTGCTCCACGCGCGGAG 537  
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Db 271 CAGGTCATGATGGGAGCGCCGCGTGGCGGAGCTGCTGCTCCACGCGCGGAG 330  
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QY 538 CCACACTGGCAGACCTGCCACTCTCACCCGACCGGCTGCATGATGCTGCCGAGGGC 597  
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Db 331 CCACACTGGCAGACCTGCCACTCTCACCCGACCGGCTGCATGATGCTGCCGAGGGC 390  
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QY 598 TTCCTGGACACGCTGGTGTGTGACACCGGCGCGGCTGCATGATGCTGCCGAGGGC 657  
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Db 391 TTCCTGGACACGCTGGTGTGTGACACCGGCGCGGCTGCATGATGCTGCCGAGGGC 450  
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Db 511 CTGGCAGACAGCCAGGGGAGCTGACCGGAGGTTCCACAGCGCCACACAGACTTTATTT 570  
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QY 778 TCTTACCAATTTCCACACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837  
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Db 571 TCTTACCAATTTCCACACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 630  
|||||

RESULT 13  
AR062777 LOCUS AR062777 1244 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5843756.  
ACCESSION AR062777  
VERSION AR062777.1 GI:5990468  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1244)  
AUTHORS Stone,S., Jiang,P. and Kamb,A.  
TITLE Mouse MTS1 gene  
JOURNAL Patent: US 5843756-A 5 01-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..1244  
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BASE COUNT 279 a 343 c 355 g 260 t 7 others  
ORIGIN

Query Match 43.0%; Score 360; DB 5; Length 1244;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTCATGATGGGAGCGCCGCGTGGCGGAGCTGCTGCTCCACGCGCGGAG 537  
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Db 271 CAGGTCATGATGGGAGCGCCGCGTGGCGGAGCTGCTGCTCCACGCGCGGAG 330  
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QY 538 CCACACTGGCAGACCTGCCACTCTCACCCGACCGGCTGCATGATGCTGCCGAGGGC 597  
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Db 331 CCACACTGGCAGACCTGCCACTCTCACCCGACCGGCTGCATGATGCTGCCGAGGGC 390  
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QY 598 TTCCTGGACACGCTGGTGTGTGACACCGGCGCGGCTGCATGATGCTGCCGAGGGC 657  
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QY 658 TGGGTCGCTGCTGCCGTGACTTGGCCGAGGAGCGGGCCACCGGACCTTGCAGGGTAC 717  
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QY 778 TCTTACCCCAATTTCCCAACCCCAACCACTTAATTCGATGAAGGCTGCCAACGGGAGCGG 837  
Db 571 TCTTACCCCAATTTCCCAACCCCAACCACTTAATTCGATGAAGGCTGCCAACGGGAGCGG 630  
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LOCUS I41151  
DEFINITION Sequence 5 from patent US 5624819.  
ACCESSION I41151  
VERSION I41151.1 GI:2081741  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1244)  
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.  
TITLE Germ-line mutations in the MTS gene  
JOURNAL Patent: US 5624819-A 5 29-APR-1997;  
FEATURES  
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BASE COUNT 279 a 343 c 355 g 260 t 7 others  
ORIGIN  
Query Match 43.0%; Score 360; DB 5; Length 1244;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTATGATGATGGGAGCGCCCGCTGGCGAGCTGCTGTCTCCACGCGCGGAG 537  
Db 271 CAGGTATGATGATGGGAGCGCCCGCTGGCGAGCTGCTGTCTCCACGCGCGGAG 330  
QY 538 CCCAATGCGCAGACCTGCCACTCTACCCGACCGCGTGATGCTGCCCGGGAGGCG 597  
Db 331 CCCAATGCGCAGACCTGCCACTCTACCCGACCGCGTGATGCTGCCCGGGAGGCG 390  
QY 598 TTCCTGGACACGCTGCTGTGTGCTGCACCGCGCGCGGCGGCTGGACGCTGCGCGATGCC 657  
Db 391 TTCCTGGACACGCTGCTGTGTGCTGCACCGCGCGCGGCGGCTGGACGCTGCGCGATGCC 450  
QY 658 TGGGTCGCTGCCGTGACTTGGCCGAGGAGCGGGCCACCGGACGTTGCAGGGTAC 717  
Db 451 TGGGGTCGCTGCCGTGACTTGGCCGAGGAGCGGGCCACCGGACGTTGCAGGGTAC 510  
QY 718 CTGCGCACAGCCACGGGGGACTGACGCCAGGTTCGCCAGCGGCCCAACAGCACTTTATT 777  
Db 511 CTGCGCACAGCCACGGGGGACTGACGCCAGGTTCGCCAGCGGCCCAACAGCACTTTATT 570  
QY 778 TCTTACCCCAATTTCCCAACCCCAACCACTTAATTCGATGAAGGCTGCCAACGGGAGCGG 837  
Db 571 TCTTACCCCAATTTCCCAACCCCAACCACTTAATTCGATGAAGGCTGCCAACGGGAGCGG 630

RESULT 15  
LOCUS AF058758 2147 bp DNA PRI 29-JAN-2000  
DEFINITION Homo sapiens cyclin-dependent kinase inhibitor 2B (CDKN2B) gene,  
partial cds.  
ACCESSION AF058758  
VERSION AF058758.1 GI:6808470  
KEYWORDS human.  
SOURCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Hominoidea; Homidae; Homo.  
REFERENCE 1 (bases 1 to 2147)  
AUTHORS Murthy,S.K. and Demetrick,D.J.  
TITLE Direct Submission  
JOURNAL Submitted (09-APR-1998) Pathology and Oncology, University of  
Calgary, 3330 Hospital Drive, N.W., Calgary, Alberta T2N 1N4,  
Canada  
FEATURES  
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/product="cyclin-dependent kinase inhibitor 2B"  
2105..>2147  
/gene="CDKN2B"  
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/product="cyclin-dependent kinase inhibitor 2B"  
/protein\_id="AAF28397.1"  
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/translation="MREENKMPSGGGS"  
BASE COUNT 589 a 495 c 512 g 551 t  
ORIGIN

Query Match 39.5%; Score 330.4; DB 39; Length 2147;  
Best Local Similarity 98.4%; Pred. No. 9.4e-46;  
Matches 366; Conservative 0; Mismatches 1; Indels 5; Gaps 3;  
QY 1 GAGGACTCCGCGACG-GTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCC 59  
Db 1779 GAGGACTCCGCGACGCTCCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCC 1838  
QY 60 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCCCGCTGGTTCCTTGAGCGCAGG 119  
Db 1839 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCCCGCTGGTTCCTTGAGCGCAGG 1898  
QY 120 AAAGCCCGGAGCTAACGACCGCGCTCGG-CACTGACAGGGGCCCCAAGCGCAGAG 178  
Db 1899 AAAGCCCGGAGCTAACGACCGCGCTCGGCACTGCGCGGCGCCCAAGCGC---AG 1955  
QY 179 AAGGACGCGGAGGCTAATGAGCTGAGCCAGGTCCTTAGGAGGAGAGAGTCCGCC 238  
Db 1956 AAGGACGCGGAGGCTAATGAGCTGAGCCAGGTCCTTAGGAGGAGAGAGTCCGCC 2015  
QY 239 GGAGCAGCGTGGGAAGAAGGAAGTGTCTTAAGTTTACGGCCCAACGGTGGATTATC 298  
Db 2016 GGAGCAGCGTGGGAAGAAGGAAGTGTCTTAAGTTTACGGCCCAACGGTGGATTATC 2075  
QY 299 CGGGCCGCTGCGGCTCTGGGGCTGCGGAATGCGCGAGGAGAACAGGCGATCCCGCAGTG 358  
Db 2076 CGGGCCGCTGCGGCTCTGGGGCTGCGGAATGCGCGAGGAGAACAGGCGATCCCGCAGTG 2135  
QY 359 GGGGGGCGGAGCG 370  
Db 2136 GGGGGGCGGAGCG 2147

Search completed: July 21, 2000, 06:05:24  
Job time: 14858 sec





Result No.	Score	Query		Length	DB	ID	Description
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2	677.2	80.9	751	1	T00745	Multiple tumour su	
3	677.2	80.9	751	1	Q98165	Human multiple tum	
4	677.2	80.9	751	1	T69781	Human multiple tum	
5	677.2	80.9	751	1	V11250	Human MTS2 cDNA. D	
6	677.2	80.9	751	1	V53831	Coding sequence 2	
7	677.2	80.9	751	1	V70595	CDNA encoding a hu	
8	360	43.0	1244	1	T00741	Multiple tumour su	
9	360	43.0	1244	1	Q98168	Human MTS2 DNA inc	
10	360	43.0	1244	1	V11241	Human MTS2 genomic	
11	360	43.0	1244	1	V53822	Nucleotide sequenc	
12	360	43.0	1244	1	V70586	Human multiple tum	
13	276.8	33.1	580	1	T02964	Cell-cycle regulat	
14	271.4	32.4	782	1	X26234	Truncated p27/p16	
15	271.4	32.4	1073	1	X26232	Truncated p27/p16	
16	266.8	31.9	471	1	V11238	Human MTS1 cDNA. D	
17	266.8	31.9	471	1	V53819	Nucleotide sequenc	
18	266.8	31.9	471	1	V70583	CDNA encoding a hu	
19	266.8	31.9	737	1	X26233	Truncated p27/p16	
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21	266.8	31.9	947	1	V11370	Human MTS1 cDNA va	
22	266.8	31.9	947	1	V53951	Coding sequence 3	
23	266.8	31.9	947	1	V70815	CDNA encoding a hu	
24	266.8	31.9	987	1	T60951	Tumour suppressor	
25	266.8	31.9	1028	1	X26331	Truncated p27/p16	
26	266.8	31.9	1098	1	T74053	CDK inhibitory fus	
27	266.8	31.9	1098	1	X26224	Human p16p27 fusio	
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29	266.8	31.9	1143	1	T74052	CDK inhibitory fus	
30	266.8	31.9	1143	1	X26223	Human p16(GS)p27 f	
31	285.6	31.7	1420	1	T74051	CDK inhibitory fus	
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Multiple tumour su  
Human multiple tum  
Human multiple tum  
Human multiple tum  
Human multiple tum  
Multiple tumour su  
Inhibitor of cycli  
Cell-cycle regulat  
Multiple tumour su  
Multiple tumour su  
Multiple tumour su  
Multiple tumour su  
Human MRS polypept  
Human multiple tum  
Human multiple tum

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Db 191 GACACGGGAGGTAATGAAGCTAGCCAGGTCTCTAGGAAGAGAGAGTGCAGCGG 250
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Qy 301 GCCCGCTCGCGTCTGGGGGCTGCGGAATGCGGAGGAGAAACAGGGCATGCCAGTGG 360
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Qy 361 GCGGACAGGATGAGGCTGCGCCA--CGCGCGCGCGGAGTCTAGTGAAGTGCGA 417
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Db 551 CCCAACTCGGAGACCTGCGCACTCTACCGGACCGGTCATGCTGCTGCGGAGGCG 610
Qy 598 TTCCTGGACACGCTGCTGCTGTCACCGGCGCGGCGCGGTCGAGCTGCGCGATGCC 657
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Qy 658 TGGGCTGCTGCTGCTGCTGCTGTCACCGGCGCGGCGCGGTCGAGCTGCGAGGCTAC 717
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Db 731 CTGCGACAGCAGCGGAGTCTGACCGAGTTCCTCCAGCGCGCCACACAGCTTTATT 790
Qy 778 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837
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## RESULT 2

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AC T00745;
DE 08-MAY-1996 (first entry).
DE Multiple tumour suppressor 2 (MTS2) gene ORF.
KW Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; open reading frame; ORF; ds.
OS Homo sapiens.
PH Key Location/Qualifiers
FT cds 335..751
FT /*tag= a
PN WO9525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 95-344626/44.
DR P-PSDB; R81702.
PT Detecting polymorphism associated with cancer pre:disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
```

```
PS Disclosure; Pages 102-103; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to the MTS2
CC gene ORF T00745 (which encodes R81702). The above assay can also be
CC used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia
CC and pancreas, breast and thyroid cancers, etc..
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
```

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Query Match 80.9%; Score 677.2; DB 1; Length 751;
Best Local Similarity 97.9%; Pred. No. 8.4e-137;
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;
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Qy 1 GAGGACTCCGCGAGC-GTCCGCACCCCTGCGGCCACAGCGGCTTTGAGTCGGCTGCTTC 59
Db 9 GAGGACTCCGCGAGCGCTCCGACCCCTGCGGCCACAGCGGCTTTGAGTCGGCTGCTTC 68
Qy 60 GCGTAGTCGCGCTTTTCCAGAGCAATCCAGGCGCGCGCTGGTCTTTGAGGCGCCAGG 119
Db 69 GCGTAGTCGCGCTTTTCCAGAGCAATCCAGGCGCGCGCTGGTCTTTGAGGCGCCAGG 128
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Db 186 AAGGACGACGGGAGGTAATGAAGCTGAGCCAGCTCTCTAGGAAGAGAGAGTGGGCC 245
Qy 239 GGACGACGCTGGGAAAGAAAGAGAGAGTGTCTTAAGTTTACGCCCAACGGTGGATTATC 298
Db 246 GGACGACGCTGGGAAAGAAAGAGAGAGTGTCTTAAGTTTACGCCCAACGGTGGATTATC 305
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Db 306 CGGCGCCTGCGCTCTGGGGCTGCGGAATGCGGAGGAGAAACAGGATGCCAGTG 365
Qy 359 GGGCGCGCAGCGATGAGGGTCTGGCCA---CGCGCGCGCGGGGACTAGTGGAGAGAGTGC 415
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Qy 416 GACACTCTGGGAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGCGGA 475
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Db 666 CTGGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGCGGCGCACCGGACGCTTGCAGGGT 725
Qy 716 ACCTGCGCAGACCCACGGGGGACTGA 741
Db 726 ACCTGCGCAGACCCACGGGGGACTGA 751
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## RESULT 3

```
Q99165
ID Q99165 standard; cdna; 751 BP.
AC Q99165;
DE 03-MAY-1996 (first entry)
DE Human multiple tumour suppressor polypeptide, MTS2 encoding cdna.
```

KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;  
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;  
OS gene therapy; chronic; ds.  
FH Homo sapiens.  
FT Key Location/Qualifiers  
FT cds 335..751  
FT /\*tag= a  
FT /product= MTS2  
PN W09525429-A1.  
PD 28-SEP-1995.  
PF 17-MAR-1995; U03316.  
PR 18-MAR-1994; US-214581.  
PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215088.  
PR 18-MAR-1994; US-215087.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Kamb A;  
DR WPI; 95-344401/44.  
DR P-PSDB; R80948.  
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences  
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.  
PT melanoma or leukaemia  
PS Claim 3; Page 102-103; 156pp; English.  
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)  
CC polypeptides have been isolated and sequenced. This sequence encodes  
CC the MTS polypeptide MTS2 (R80948). MTS polypeptide-encoding cDNAs  
CC and mutants of these are useful for the diagnosis or prognosis of  
CC human cancer. Germ-line mutations of MTS cDNAs can be used for  
CC diagnosing predisposition to melanoma, leukaemia, astrocytoma,  
CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers  
CC of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and  
CC rectum. The wild-type gene is useful for gene therapy and MTS  
CC polypeptides may also be used for protein replacement therapy. Also  
CC the polypeptides or cells contg. an altered MTS gene are useful for  
CC screening for potential cancer therapeutics.  
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

Query Match 80.9%; Score 677.2; DB 1; Length 751;  
Best Local Similarity 97.9%; Pred. No. 8.4e-137;  
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

QY 1 GAGGACTCCGCGAGC-GTCCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC 59  
DB 9 GAGGACTCCGCGAGCGCTCCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC 68  
QY 60 GCGTAGGCGCTTTTCCAGAGCAATCCAGCGCGCGCCCGCTGCTTCCAGCGCCAGG 119  
DB 69 GCGTAGGCGCTTTTCCAGAGCAATCCAGCGCGCGCCCGCTGCTTCCAGCGCCAGG 128  
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DB 129 AAAGCCCGGAGCTAACGACCGCGCGCTCGGCACTGCACGGCGGCCCAAGCCAGG 185  
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DB 186 AAGGACGACGGGAGGTAATGAAGCTGAGCCAGCTCTCTAGGAAGAGAGAGTGCGCC 245  
QY 239 GGAGCAGCGTGGGAAGAGAGAGTGCTGTTAAGTTTACGCGCAACGGTGATATC 298  
DB 246 GGAGCAGCGTGGGAAGAGAGAGTGCTGTTAAGTTTACGCGCAACGGTGATATC 305  
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DB 306 CGGCGCGCTGCGCTCTGGGGCTCGGAATCCGCGAGGAGCAAGGGCATGCCAGTG 365  
QY 359 GGGCGCGGAGGAGGAGGCTTGGGCA--CGCGCGCGGGGAGTACTGTGAGAGAGGTGC 415  
DB 366 GGGCGCGGAGGAGGAGGCTTGGGCACTGCGCGCGGGGAGTACTGTGAGAGAGGTGC 425

QY 416 GACACTCTCTGGGAAGCGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGGCGCGCGA 475  
DB 426 GACAGCTCTCTGGGAAGCGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGGCGCGCGA 485  
QY 476 TCAGAGTCATGATGATGGGAGCGCGCGCTGGGGAGCTGCTGCTCTCCACGGCGCGG 535  
DB 486 TCAGAGTCATGATGATGGGAGCGCGCGCTGGGGAGCTGCTGCTCTCCACGGCGCGG 545  
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DB 546 AGCCCAACTGCGAGACCCCTGCCACTCTCACCCGACCGGTCATGATGCTGCCCGGAGG 605  
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DB 606 GCTTCCTGGACACGCTGGTGGTGTGCTGACCGGGCGCGCGCGCTGGAGCTGGCGCATG 665  
QY 656 CTTGGGCTGCTCTGCCCTGGACTTGGCCGAGGAGCGGGGCCACCGGACGCTTTCAGAGGT 715  
DB 666 CTTGGGCTGCTCTGCCCTGGACTTGGCCGAGGAGCGGGGCCACCGGACGCTTTCAGAGGT 725  
QY 716 ACTGCGCACAGCACCGGGGAGCTGA 741  
DB 726 ACTGCGCACAGCACCGGGGAGCTGA 751

RESULT 4  
T69781  
ID T69781 standard; cDNA; 751 BP.  
AC T69781;  
DT 10-SEP-1997 (first entry)  
DE Human multiple tumour suppressor gene 2.  
KW Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FH cds 335..751  
FT /\*tag= a  
FT US5624819-A.  
PN 29-APR-1997.  
PD 18-MAR-1994; 214582.  
PF 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215087.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PR 17-MAR-1995; WO-003537.  
PR 07-JUN-1995; US-474177.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (UTAH ) UNIV UTAH RES. FOUND.  
PI Cannon-Albright LA, Kamb A, Skolnick MH;  
DR WPI; 97-258217/23.  
DR P-PSDB; W19255.  
PT Human mutant multiple tumour suppressor gene sequences - for  
PT production of recombinant mutant polypeptide(s)  
PS Disclosure: Columns 75-78; 72pp; English.  
CC The present sequence the human multiple tumour suppressor gene 2  
CC (MTS2), useful in cancer diagnosis.  
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

Query Match 80.9%; Score 677.2; DB 1; Length 751;  
Best Local Similarity 97.9%; Pred. No. 8.4e-137;  
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

QY 1 GAGGACTCCGCGAGC-GTCCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC 59  
DB 9 GAGGACTCCGCGAGCGCTCCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC 68  
QY 60 GCGTAGGCGCTTTTCCAGAGCAATCCAGCGCGCGCCCGCTGCTTCCAGCGCCAGG 119  
DB 69 GCGTAGGCGCTTTTCCAGAGCAATCCAGCGCGCGCCCGCTGCTTCCAGCGCCAGG 128  
QY 120 AAAGCCCGGAGCTAACGACCGCGCGCTCGG-CACTGCACGGCGGCCCAAGCCAGAG 178  
DB 129 AAAGCCCGGAGCTAACGACCGCGCGCTCGGCACTGCACGGCGGCCCAAGCCAGG 185





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Db 69 GCGTAGGCGCTTTTCCCAAGAACAAATCAGGGCGCGCCCGCTGGTCTTGTAGCGCCAGG 128
Qy 120 AAAAGCCCGGAGCTAACACCGCGCGCTCGG-CAGTGCACGGGGCCCAAGCCGCAAG 178
    |||||
Db 129 AAAAGCCCGGAGCTAACACCGCGCGCTCGGCACTGCACGGGGCCCAAGCGC---AG 185
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Qy 179 AAGGACGACGGGAGGTAATGAAGCTGAGCCCAAGTCTCTTAGAAGAGAGAGTCCGCC 238
    |||||
Db 186 AAGGACGACGGGAGGTAATGAAGCTGAGCCCAAGTCTCTTAGAAGAGAGAGTCCGCC 245
    |||||
Qy 239 GGAGCAGCTGGGAAGAGGAGAGTGTCTTAAGTTTACGCCCAACGGTGGATTATC 298
    |||||
Db 246 GGAGCAGCTGGGAAGAGGAGAGTGTCTTAAGTTTACGCCCAACGGTGGATTATC 305
    |||||
Qy 299 CGGCGCCCTCGCGCTCTGCGGCTGCGGAATGCGGAGAGAACAGAGGCGATCCCGAGT 358
    |||||
Db 306 CGGCGCCCTCGCGCTCTGCGGCTGCGGAATGCGGAGAGAACAGAGGCGATCCCGAGT 365
    |||||
Qy 359 GGGCGCGCAGGATGAGGGTCTGGCCA---CGCGCGCGGGGAGTGTGGAGAGGTGC 415
    |||||
Db 366 GGGCGCGCAGGATGAGGGTCTGGCCAAGCGCGCGCGGGGAGTGTGGAGAGGTGC 425
    |||||
Qy 416 GACACTCTCTGGAAGCGCGCGGATGCCCAACGAGTCAACCGTTTCGGGAGCGCGCGA 475
    |||||
Db 426 GACAGCTCTCTGGAAGCGCGCGGATGCCCAACGAGTCAACCGTTTCGGGAGCGCGCGA 485
    |||||
Qy 476 TCCAGGTATGATGAGGAGCGCGCGCGCTGCGGAGTGTCTGCTCCACGCGCGCGG 535
    |||||
Db 486 TCCAGGTATGATGAGGAGCGCGCGCGCTGCGGAGTGTCTGCTCCACGCGCGCGG 545
    |||||
Qy 536 AGCCCACTGCGCAGACCTTGCACATCTCACCGACCGGTGCATGTCTGCCCGGAGG 595
    |||||
Db 546 AGCCCACTGCGCAGACCTTGCACATCTCACCGACCGGTGCATGTCTGCCCGGAGG 605
    |||||
Qy 596 GCTTCTGGACACGCTGGTGTGTGTCACCGCGCGGGCGCGCTGGAGTGCAGTGCAGG 655
    |||||
Db 606 GCTTCTGGACACGCTGGTGTGTGTCACCGCGCGGGCGCGCTGGAGTGCAGTGCAGG 665
    |||||
Qy 656 CTGGGGTGTCTGCGCTGAGCTTGGCCGAGGAGCGGGGCCACCGCGAGCTTTCAGGTT 715
    |||||
Db 666 CTGGGGTGTCTGCGCTGAGCTTGGCCGAGGAGCGGGGCCACCGCGAGCTTTCAGGTT 725
    |||||
Qy 716 ACCTGCGCAGACCGCGGGGACTGA 741
    |||||
Db 726 ACCTGCGCAGACCGCGGGGACTGA 751
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```

## RESULT 8

```
T00741
ID T00741 standard; DNA; 1244 BP.
AC T00741;
DT 08-MAY-1996 (first entry)
DE Multiple tumour suppressor 2 (MTS2) gene exon 2 contg. fragment.
KW Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; exon 2; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT intron 1..273
    /tag= a
    /label= intron 1
FT exon 274..529
    /tag= b
    /label= exon 2
FT intron 530..1244
    /tag= c
    /label= intron 2
FT PN W09525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
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PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 95-344626/44.
PT Detecting polymorphism associated with cancer pre:disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Example 6: Page 96; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to exon 2
CC (T00741) of the MTS2 gene. The above assay can also be used in the
CC diagnosis and prognosis of melanoma, lymphoma, leukaemia and
CC pancreas, breast and thyroid cancers, etc.
SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;
```

Query Match 43.0%; Score 360; DB 1; Length 1244;

Best Local Similarity 100.0%; Pred. NO. 6.2e-69;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 478 CAGGTCATGATGAGGCGCGCGCGCTGCGGAGCTGCTGCTCCACGGCGCGAG 537
    |||||
Db 271 CAGGTCATGATGAGGCGCGCGCGCTGCGGAGCTGCTGCTCCACGGCGCGAG 330
    |||||
Qy 538 CCCAACTCGCAGACCTTGCACACTCTCACCGACCGGTGCATGTCTGCCCGGAGGCG 597
    |||||
Db 331 CCCAACTCGCAGACCTTGCACACTCTCACCGACCGGTGCATGTCTGCCCGGAGGCG 390
    |||||
Qy 598 TTCCTGGACACGCTGGTGTGCTGCACCGCGCGGGCGCGGTGGACGTGCGCGATGCC 657
    |||||
Db 391 TTCCTGGACACGCTGGTGTGCTGCACCGCGCGGGCGCGGTGGACGTGCGCGATGCC 450
    |||||
Qy 658 TGGGTCGCTGCGCGCTGGACTTGGCCGAGAGCGCGGCCACCGAGCTTGCAGGGTAC 717
    |||||
Db 451 TGGGTCGCTGCGCGCTGGACTTGGCCGAGAGCGCGGCCACCGAGCTTGCAGGGTAC 510
    |||||
Qy 718 CTGGCAGACGACGGGGAGTACGCGCAGGTTCCCGAGCGCGCCACACAGACTTTATTT 777
    |||||
Db 511 CTGGCAGACGACGGGGAGTACGCGCAGGTTCCCGAGCGCGCCACACAGACTTTATTT 570
    |||||
Qy 778 TCTTACCAATTTCCACCCCGCCACCTTAATTCGATGAAGGCTGCCACGGGGAGCGG 837
    |||||
Db 571 TCTTACCAATTTCCACCCCGCCACCTTAATTCGATGAAGGCTGCCACGGGGAGCGG 630
    |||||
```

## RESULT 9

Q99168

ID Q99168 standard; cDNA; 1244 BP.

AC Q99168;

DT 07-MAY-1996 (first entry)

DE Human MTS2 DNA including exon 2, intron 2 and part of intron 1.

KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;

KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;

KW gene therapy; chronic; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT intron 1..273

/tag= a

/number= 1

/label= 274..580

FT exon 274..580

/tag= b

/number= 1

/label= 581..1244

FT intron 581..1244

/tag= c

/number= 2

FT PN W09525429-A1.

PD 28-SEP-1995.

PF 17-MAR-1995; U03316.

PR 18-MAR-1994; US-214581.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215088.  
PR 18-MAR-1994; US-215087.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Kamb A;  
DR WPI: 95-344401/44.  
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences  
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.  
PT melanoma or leukaemia  
PS Example 6: Page 96; 156pp; English.  
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)  
CC polypeptides have been isolated and sequenced. This sequence includes  
CC intron 2, exon 2 and part of intron 1 of the MTS polypeptide, MTS2. MTS  
CC polypeptide-encoding cDNAs and mutants of these are useful for the  
CC diagnosis or prognosis of human cancer. Germ-line mutations of MTS  
CC cDNAs can be used for diagnosing predisposition to melanoma, leukaemia,  
CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL  
CC and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney,  
CC stomach and rectum. The wild-type gene is useful for gene therapy and  
CC MTS polypeptides may also be used for protein replacement therapy. Also  
CC the polypeptides or cells contg. an altered MTS gene are useful for  
CC screening for potential cancer therapeutics.  
SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;  
Best Local Similarity 100.0%; Pred. No. 6.2e-69;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 537  
DB 271 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 330  
QY 538 CCCAACTGGCGAGACCTGCCACTCTCACCCGCGGTGCATGCTGCCCGGGAGGCG 597  
DB 331 CCCAACTGGCGAGACCTGCCACTCTCACCCGCGGTGCATGCTGCCCGGGAGGCG 390  
QY 598 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 657  
DB 391 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 450  
QY 658 TGGGGTGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCGAGGTAC 717  
DB 451 TGGGGTGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCGAGGTAC 510  
QY 718 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCGCCAGCGCCCAACAGCTTTATTT 777  
DB 511 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCGCCAGCGCCCAACAGCTTTATTT 570  
QY 778 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837  
DB 571 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 630

RESULT 10  
V11241  
ID V11241 standard; DNA; 1244 BP.  
AC V11241;  
DT 15-JUL-1998 (first entry)  
DE Human MTS2 genomic DNA including exon 2.  
KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;  
KW familial melanoma locus; MLM; predisposition; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Intron 1..273  
FT /\*tag= a  
FT /number= 1  
FT exon 274..529  
FT /\*tag= b  
FT /number= 2  
FT /note= "Corresponds to exon 2 in V11240"

PN US5739027-A.  
PD 14-APR-1998.  
PF 07-JUN-1995; 487033.  
PR 07-JUN-1995; US-487033.  
PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215087.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PR 17-MAR-1995; WO-U03316.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Kamb A;  
DR WPI: 98-250421/22.  
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are  
PT useful for the diagnosis of cancers related to MTS1E1-beta  
PT mutation(s) and their treatment  
PS Disclosure: Fig 7; 72pp; English.  
CC This sequence encodes the human multiple tumour suppression protein,  
CC MTS1, exon 2. The MTS gene locus is also referred to as the familial  
CC melanoma (FML) gene locus, located on human chromosome 9p21. Germ line  
CC mutations in MTS genes can be used in the diagnosis of predisposition to  
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,  
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,  
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum.  
SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;  
Best Local Similarity 100.0%; Pred. No. 6.2e-69;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 537  
DB 271 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 330  
QY 538 CCCAACTGGCGAGACCTGCCACTCTCACCCGCGGTGCATGCTGCCCGGGAGGCG 597  
DB 331 CCCAACTGGCGAGACCTGCCACTCTCACCCGCGGTGCATGCTGCCCGGGAGGCG 390  
QY 598 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 657  
DB 391 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 450  
QY 658 TGGGGTGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCGAGGTAC 717  
DB 451 TGGGGTGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCGAGGTAC 510  
QY 718 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCGCCAGCGCCCAACAGCTTTATTT 777  
DB 511 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCGCCAGCGCCCAACAGCTTTATTT 570  
QY 778 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837  
DB 571 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 630

RESULT 11  
V53822  
ID V53822 standard; cDNA; 1244 BP.  
AC V53822;  
DT 04-DEC-1998 (first entry)  
DE Nucleotide sequence of the multiple tumour suppressor 2.  
KW Multiple tumour suppressor 2; MTS-2; human; cancer; hybridisation;  
KW somatic mutation; gene therapy; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Intron 1..273  
FT /\*tag= a  
FT /note= "intron 1"  
FT US5801236-A.  
PD 01-SEP-1998.  
PF 07-JUN-1995; 480810.  
PR 07-JUN-1995; US-480810.



PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215086.  
PR 18-MAR-1994; US-215087.  
PR 14-APR-1994; US-227369.  
PR 01-JUN-1994; US-251938.  
PR 17-MAR-1995; WO-U03316.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Kamb A;  
DR WPI; 98-494842/42.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
PS Disclosure; Fig 7A-7B; 73pp; English.

CC This is the nucleotide sequence of the multiple tumour suppressor 2  
CC (MTS-2) gene, used in the method of the invention. The MTS gene  
CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
CC standard nucleic hybridisation techniques, of patient samples. The  
CC mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.

SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;

Best Local Similarity 100.0%; Pred. No. 6.2e-69;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGTCTCATGATGGCGAGCGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 537

Db 271 CAGTCTCATGATGGCGAGCGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 330

QY 538 CCCAACTGCGGAGACCTGCGACTCTCACCAGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 597

Db 331 CCCAACTGCGGAGACCTGCGACTCTCACCAGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 390

QY 598 TTCCTGGACAGCTGTGGTGTCTGACCGCGCGGCGGCGGCGTGGACGTGCGCGATGCC 657

Db 391 TTCCTGGACAGCTGTGGTGTCTGACCGCGCGGCGGCGGCGTGGACGTGCGCGATGCC 450

QY 658 TGGGGTGTGTCGCCGTGGACTTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 717

Db 451 TGGGGTGTGTCGCCGTGGACTTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 510

QY 718 CTGGCGACAGCGGGGGACTGACGCCAGCTTAATTCGATGAAGGCTGCCAAGCGGAGCGG 777

Db 511 CTGGCGACAGCGGGGGACTGACGCCAGCTTAATTCGATGAAGGCTGCCAAGCGGAGCGG 570

QY 778 TCTTACCAATTTCCACCCCGGAGTGTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 837

Db 571 TCTTACCAATTTCCACCCCGGAGTGTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 630

RESULT 12

V70586

ID V70586 standard; DNA; 1244 BP.

AC V70586; 1999 (first entry)

DE Human multiple tumour suppressor 2 (MTS2) DNA fragment.

KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT intron 1..273

FT exon /\*tag= a

FT exon 274..529

FT exon /\*tag= b

FT /\*note= "corresponds to the exon of V70585"

PN US5843756-A.

PD 01-DEC-1998.  
PF 28-JUL-1995; 058735.  
PR 28-JUL-1995; US-508735.  
PR 07-JUN-1995; US-487033.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Jiang P, Kamb A, Stone S;  
DR WPI; 99-044585/04.

PT Mouse multiple tumour suppressor gene segment - useful for primer  
PT design

PS Example 6; Fig 7A-B; 80pp; English.

CC The present sequence represents part of intron 1, exon 2 and intron  
CC 2 for a human multiple tumour suppressor 2 (MTS2) gene. The  
CC MTS1 sequence is homologous to the corresponding murine gene.

CC Primers designed from the gene can be used to design primers to  
CC detect abnormalities i.e. polymorphisms which may predispose towards  
CC malignancies such as melanoma, leukaemia, astrocytoma, lymphoma,  
CC glioma, as well as tumours of e.g. the breast, thyroid, pancreas,  
CC uterus and kidneys.

SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;

Best Local Similarity 100.0%; Pred. No. 6.2e-69;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGTCTCATGATGGCGAGCGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 537

Db 271 CAGTCTCATGATGGCGAGCGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 330

QY 538 CCCAACTGCGGAGACCTGCGACTCTCACCAGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 597

Db 331 CCCAACTGCGGAGACCTGCGACTCTCACCAGCCGCGTGGCGAGTGTCTGCTCCACGCGCGGAG 390

QY 598 TTCCTGGACAGCTGTGGTGTCTGACCGCGCGGCGGCGGCGTGGACGTGCGCGATGCC 657

Db 391 TTCCTGGACAGCTGTGGTGTCTGACCGCGCGGCGGCGGCGTGGACGTGCGCGATGCC 450

QY 658 TGGGGTGTGTCGCCGTGGACTTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 717

Db 451 TGGGGTGTGTCGCCGTGGACTTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 510

QY 718 CTGGCGACAGCGGGGGACTGACGCCAGCTTAATTCGATGAAGGCTGCCAAGCGGAGCGG 777

Db 511 CTGGCGACAGCGGGGGACTGACGCCAGCTTAATTCGATGAAGGCTGCCAAGCGGAGCGG 570

QY 778 TCTTACCAATTTCCACCCCGGAGTGTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 837

Db 571 TCTTACCAATTTCCACCCCGGAGTGTGGCGAGAGCGGGGCCACCGCGAGTGTGCGAGGGTAC 630

RESULT 13

T02964

ID T02964 standard; cDNA; 580 BP.

AC T02964;

DT 01-MAR-1996 (first entry)

DE Cell-cycle regulatory protein p15 cDNA.

KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;

KW CCR; gene therapy; transgenic animal; cancer; cell proliferation;

KW ss; ds.

OS Mus sp.

FH Key Location/Qualifiers

FT cds 91..483

FT /\*tag= a

PN W09528483-A1.

PD 26-OCT-1995.

PF 14-APR-1995; U04636.

PR 14-APR-1994; US-227371.

PR 25-MAY-1994; US-248812.

PR 14-SEP-1994; US-306511.

PR 29-NOV-1994; US-346147.

PA (COLD-) COLD SPRING HARBOR LAB.

PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;

DR WPI; 95-373798/48.





KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
KW tachycardia; human; p27; p16; truncated; ss.  
OS Homo sapiens.  
PN W09906540-A2.  
PD 11-FEB-1999.

PF 29-JUL-1998; U15759.  
PF 29-JUL-1997; US-902572.

PA (MITO-) MITOX INC.

PI Beach DH, Gyuris J, Lamphere L;

DR WPI; 99-153770/13.

PT fusion and chimeric proteins including cyclin-dependent kinase

PT binding motif - used for regulation of cell proliferation and

PT differentiation, for treatment of, e.g. vascular injury, cancers,

PT fibrosis and neurodegeneration

PS Claim 60; Page 83-84; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases  
(CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
transfection system (A) that comprises: (i) first gene construct  
comprising a sequence encoding an inhibitory polypeptide containing at  
least one CDK-binding motif for binding and inhibiting activity of a CDK,  
linked to a transcription regulator functional in eukaryotic cells; (ii)  
second gene construct comprising a sequence encoding a polypeptide that  
promotes endothelialisation, and (iii) a gene delivery composition for  
delivering the GCs to a cell for transfection. Also provided are nucleic  
acids encoding a fusion protein (FP) containing: (i) a therapeutic  
polypeptide sequence (TP) from an intracellular protein that alters a  
cellular process when FP enters the cell, and (ii) a transcellular  
polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
consists of at least one CDK-binding motif and a TCP. See X26220 for  
detailed uses of the recombinant transfection system. The present  
CC sequence represents a DNA encoding a human truncated p27/pl6 fusion  
protein.

SQ Sequence 1073 BP; 215 A; 317 C; 388 G; 153 T;

Query Match 32.48; Score 271.4; DB 1; Length 1073;  
Best Local Similarity 77.6%; Pred. No. 5.5e-50;  
Matches 342; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

QY 301 GGCCGCTCGGCTGCGGGCTGCGGATGCGCGAGGAGACAAAGGCGATGCCCGAGTGGG 360  
DB 562 GGGGTGCGGTTGCGGGGGTGGATCCGTCGAGGATCCGCGCGGGGAGGAGCGATG 621  
QY 361 GGCGGACGATGAGGGTCTGGCCACG---CCGGCGGGGAGCTAGTGAGAGGTCGGA 417  
DB 622 GAGCCTTCGGCTGACTGCTGGCCACGCGCGCGCGGGTGGGTAGAGGAGTGGG 681  
QY 418 CACTCTGGGAAGCGGGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGGCGCGATC 477  
DB 692 GCGTGTGAGAGCGGGGGCGCTGCCCAACACACCGAATAGTTACGTCGGAGGCGGATC 741  
QY 478 CAGGTCATGATGAGGCGAGCGCGCGTGGCGGAGTCTGCTGCTCCACGCGCGGAG 537  
DB 742 CAGGTCATGATGAGGCGAGCGCGGAGTGGCGGAGTCTGCTCTCCACGCGCGGAG 801  
QY 538 CCCAACTCGGACACCTTGCACCTCTCACCGACCGGTGATGATGCTGCCCGGAGGGC 597  
DB 802 CCCAACTCGGCGGACCCCGCACCTCTCACCGACCGGTGATGATGCTGCCCGGAGGGC 861  
QY 598 TTCCTGGACACGCTGGTGGTCTGCACCGGGCGGGCGGGTGGAGCTGCGCGATGCC 657  
DB 862 TTCCTGGACACGCTGGTGGTCTGCACCGGGCGGGCGGGTGGAGCTGCGCGATGCC 921  
QY 658 TGGGTGCTGTCGCCGTGGCTGGCGGAGGAGCGGGCCACCGCGAGCTTGCAGGGTAC 717  
DB 922 TGGGCCCGCTGCGCGGTGGACTGCTGAGGAGGCTGGGCCATCCCGATGTCGCACGGTAC 981  
QY 718 CTGGCCACAGCCAGGGGGAC 738  
DB 982 CTGGCGCGGCTGCGGGGGC 1002

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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7: /cgn2.6/pdata/1/lna/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	837	100.0	837	4	US-08-306-511A-3
2	837	100.0	837	4	US-08-893-274-3
3	812.8	97.1	850	4	US-08-627-610-3
4	812.8	97.1	850	5	US-08-581-918A-3
5	812.8	97.1	850	6	PCT-US95-04636-3
6	677.2	80.9	751	1	US-08-474-177-15
7	677.2	80.9	751	2	US-08-487-033-15
8	677.2	80.9	751	3	US-08-480-810-15
9	677.2	80.9	751	3	US-08-508-735-15
10	677.2	80.9	751	4	US-08-848-251-15
11	677.2	80.9	751	4	US-08-486-047-15
12	677.2	80.9	751	5	US-09-120-130-15
13	677.2	80.9	751	5	US-09-115-252-15
14	360	43.0	1244	1	US-08-474-177-5
15	360	43.0	1244	2	US-08-487-033-5
16	360	43.0	1244	2	US-08-480-810-5
17	360	43.0	1244	3	US-08-508-735-5
18	360	43.0	1244	4	US-08-848-251-5
19	360	43.0	1244	4	US-08-486-047-5
20	360	43.0	1244	5	US-09-120-130-5
21	360	43.0	1244	5	US-09-115-252-5
22	276.8	33.1	580	4	US-08-627-610-7
23	276.8	33.1	580	5	US-08-581-918A-7
24	276.8	33.1	580	6	PCT-US95-04636-7
25	266.8	31.9	471	1	US-08-474-177-1
26	266.8	31.9	471	2	US-08-487-033-1

27	266.8	31.9	471	2	US-08-480-810-1	Sequence 1, Appli
28	266.8	31.9	471	3	US-08-508-735-1	Sequence 1, Appli
29	266.8	31.9	471	4	US-08-848-251-1	Sequence 1, Appli
30	266.8	31.9	471	4	US-08-486-047-1	Sequence 1, Appli
31	266.8	31.9	471	5	US-09-120-130-1	Sequence 1, Appli
32	266.8	31.9	471	5	US-09-115-252-1	Sequence 1, Appli
33	266.8	31.9	947	1	US-08-474-177-36	Sequence 36, Appl
34	266.8	31.9	947	2	US-08-487-033-36	Sequence 36, Appl
35	266.8	31.9	947	2	US-08-480-810-36	Sequence 36, Appl
36	266.8	31.9	947	3	US-08-508-735-36	Sequence 36, Appl
37	266.8	31.9	947	4	US-08-848-251-36	Sequence 36, Appl
38	266.8	31.9	947	4	US-08-486-047-36	Sequence 36, Appl
39	266.8	31.9	947	5	US-09-120-130-36	Sequence 36, Appl
40	266.8	31.9	947	5	US-09-115-252-36	Sequence 36, Appl
41	265.6	31.7	1420	1	US-08-589-981-1	Sequence 1, Appli
42	265.4	31.7	393	3	US-08-508-735-45	Sequence 45, Appl
43	265.2	31.7	948	1	US-08-154-915-3	Sequence 3, Appli
44	265.2	31.7	948	6	PCT-US93-09945-3	Sequence 3, Appli
45	265.2	31.7	994	4	US-08-627-610-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-306-511A-3  
; Sequence 3, Application US/08306511A  
; Patent No. 5962316  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,511A  
; FILING DATE: 14-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 837 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 328..738  
; US-08-306-511A-3  
  
Query Match 100.0%; Score 837; DB 4; Length 837;  
Best Local Similarity 100.0%; Pred. No. 3.4e-179;



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Db 241 AGCAGCGTGGGAAGAGGAAAGTGTCGTTAAGTTTACGGCCACAGGTGGATTATCCG 300  
QY 301 GGCCGCTGCGCGTCTGGGGCTCGGAATGCGGAGAGAACAAAGGCGATGCCAGTGGG 360  
Db 301 GGCCGCTGCGCGTCTGGGGCTCGGAATGCGGAGAGAACAAAGGCGATGCCAGTGGG 360  
QY 361 GGCGGACGAGATAGGGTCTGGCCACGCGCGCGCGCGGGGACTAGTGAGAGGTGGCACAC 420  
Db 361 GGCGGACGAGATAGGGTCTGGCCACGCGCGCGCGCGGGGACTAGTGAGAGGTGGCACAC 420  
QY 421 TCTGTGGAAGCCGCGCGGATCCACAGGAGTCAACCGTTTTCGGGAGGCGCGGATCCAG 480  
Db 421 TCTGTGGAAGCCGCGCGGATCCACAGGAGTCAACCGTTTTCGGGAGGCGCGGATCCAG 480  
QY 481 GTCATGATGATGGGACGCGCGCGCGTGGCGAGCTGCTGTCTCCACGCGCGGAGGCC 540  
Db 481 GTCATGATGATGGGACGCGCGCGCGTGGCGAGCTGCTGTCTCCACGCGCGGAGGCC 540  
QY 541 AACTGCGACAGCCCTGCCACTCTACCCGACCGCGGTGCATGATGCTGCCCGGGAGGCTTC 600  
Db 541 AACTGCGACAGCCCTGCCACTCTACCCGACCGCGGTGCATGATGCTGCCCGGGAGGCTTC 600  
QY 601 CTGACACGCTGTGTGTGTCACCGCGCGCGCGCGGTGCACGTGCGCGATGCGCTGG 660  
Db 601 CTGACACGCTGTGTGTGTCACCGCGCGCGCGCGGTGCACGTGCGCGATGCGCTGG 660  
QY 661 GGTGCTGTCGCGTGGACTTTGGCCGAGGAGCGGGGCCACCGGACGTTCGAGGGTACCTG 720  
Db 661 GGTGCTGTCGCGTGGACTTTGGCCGAGGAGCGGGGCCACCGGACGTTCGAGGGTACCTG 720  
QY 721 CGCACAGCCACGGGGACTGACCCAGGTTCGCCAGCGCGGCCACCGGACGTTCGAGGGTATCT 780  
Db 721 CGCACAGCCACGGGGACTGACCCAGGTTCGCCAGCGCGGCCACCGGACGTTCGAGGGTATCT 780  
QY 781 TACCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837  
Db 781 TACCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837

RESULT 3

US-08-627-610-3  
; Sequence 3, Application US/08627610  
; Patent No. 5919997  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Depinho, Ronald A.  
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle  
; TITLE OF INVENTION: Regulation  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,610  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 850 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 338..751  
; US-08-627-610-3  
  
Query Match 97.1%; Score 812.8; DB 4; Length 850;  
Best Local Similarity 98.8%; Pred. No. 8.e-174;  
Matches 830; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
  
QY 1 GAGGACTCGCGACGGTCCGCCACCCCTGCCGCCAGAGCGGCTTTGAGCTCGGCTGCTCCG 60  
Db 11 GAGGACTCGCGACGGTCCGCCACCCCTGCCGCCAGAGCGGCTTTGAGCTCGGCTGCTCCG 70  
QY 61 CGCTAGCGGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGGTTCCTTTGAGCGCCAGGA 120  
Db 71 CGCTAGCGGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGGTTCCTTTGAGCGCCAGGA 130  
QY 121 AAAGCCCGGAGTAAAGACCGCGGCTCGGCACTGACGCGGGGCCCAAGCCCGCAGAGAA 180  
Db 131 AAAGCCCGGAGTAAAGACCGCGGCTCGGCACTGACGCGGGGCCCAAGCCCGCAGAGAA 190  
QY 181 GGNACGAGGAGGTAATGAAGCTGAGCGCCAGGTCTCTTAGNAGAGAGAGTGCGCCGG 240  
Db 191 GGACGAGGAGGTAATGAAGCTGAGCGCCAGGTCTCTTAGNAGAGAGAGTGCGCCGG 250  
QY 241 AGCAGCGTGGGAAAGAGAGTGTCTTAAGTTTACGGCCACCGTGGATTATCCG 300  
Db 251 AGCAGCGTGGGAAAGAGAGTGTCTTAAGTTTACGGCCACCGTGGATTATCCG 310  
QY 301 GGCCGCTGCGCTCTGGGGGCTGCGGAATGCGGAGGAGAACAAAGGCGATGCCAGTGGG 360  
Db 311 GGCCGCTGCGCTCTGGGGGCTGCGGAATGCGGAGGAGAACAAAGGCGATGCCAGTGGG 370  
QY 361 GGCGGACGAGTGGGCTGCGCA--CGCCGCGCGGGGACTAGTGGAGAGGTGCGGA 417  
Db 371 GGCGGACGAGTGGGCTGCGCAAGCGCGGCGGACTAGTGGAGAGGTGCGGA 430  
QY 418 CACTCTGGGAAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGATC 477  
Db 431 CAGCTCTGGAGCCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGATC 490  
QY 478 CAGGTGATGATGGGACGCGCGCGTGGGGAGCTGCTGCTCCACGCGCGGAG 537  
Db 491 CAGGTGATGATGGGACGCGCGCGTGGGGAGCTGCTGCTCCACGCGCGGAG 550  
QY 538 CCAACTGCGAGACCTGCCACTCTCACCCGCGGTCATGATGCTGCCCGGGAGGCG 597  
Db 551 CCAACTGCGAGACCTGCCACTCTCACCCGCGGTCATGATGCTGCCCGGGAGGCG 610  
QY 598 TTCTTGACACGCTGCTGCTGTCACCGCGCGCGCGGCTGGACGTGCCGATGCC 657  
Db 611 TTCTTGACACGCTGCTGCTGTCACCGCGCGCGGCTGGACGTGCCGATGCC 670  
QY 658 TGGGTGCTGCTGCGCGTGGACTTGGCCGAGGAGCGGGCCACGCGACGTTCGAGGGTAC 717  
Db 671 TGGGTGCTGCTGCGCGTGGACTTGGCCGAGGAGCGGGCCACGCGACGTTCGAGGGTAC 730  
QY 718 CTGCGACAGCCACGCGGGGACTGACCCAGGTTCGCCCGCGGCCACACGACTTTATTT 777  
Db 731 CTGCGACAGCCACGCGGGGACTGACCCAGGTTCGCCCGCGGCCACACGACTTTATTT 790  
QY 778 TCTTACCCCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837  
Db 791 TCTTACCCCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 850



APPLICATION NUMBER: PCT/US95/04636  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/346,147  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 850 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 338..751  
PCT-US95-04636-3

Query Match 97.1%; Score 812.8; DB 6; Length 850;  
Best Local Similarity 98.8%; Pred. No. 8.8e-174;  
Matches 830; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
QY 1 GAGGACTCGCGACGCTCGCCACCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCTCGG 60  
Db 11 GAGGACTCGCGACGCTCGCCACCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCTCGG 70  
QY 61 CGCTAGGCGCTTTTCCAGAGAGCAATCAGGCGCGCGCTGGTTCCTTGAGGCGCCAGGA 120  
Db 71 CGCTAGGCGCTTTTCCAGAGAGCAATCAGGCGCGCGCTGGTTCCTTGAGGCGCCAGGA 130  
QY 121 AAAGCCGGAGCTAAGCAGCGCGCTCGGCACTGCGAGCGGGCCCCAAGCCGAGAGAA 180  
Db 131 AAAGCCGGAGCTAAGCAGCGCGCTCGGCACTGCGAGCGGGCCCCAAGCCGAGAGAA 190  
QY 181 GGACGACGGAGGGTAAATGAAGCTGAGCCAGCTCTCTAGGAGAGAGAGTGCCTCCGG 240  
Db 191 GGACGACGGAGGGTAAATGAAGCTGAGCCAGCTCTCTAGGAGAGAGAGTGCCTCCGG 250  
QY 241 AGCAGCGTGGGAAGAGGAGAGTGTCTTAAGTTTACGGCCACGCTGGATTATCCG 300  
Db 251 AGCAGCGTGGGAAGAGGAGAGTGTCTTAAGTTTACGGCCACGCTGGATTATCCG 310  
QY 301 GGCCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAAAGGCGCATGCCAGTGGG 360  
Db 311 GGCCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGAGAGAAAGGCGCATGCCAGTGGG 370  
QY 361 GGCGGACGAGTGAAGGTCTGGCCA---CGCCGCGCGGGAGTACTGGAGAGAGTGCGGA 417  
Db 371 GGCGGACGAGTGAAGGTCTGGCCAGCGCGCGGCGGGAGTACTGGAGAGAGTGCGGA 430  
QY 418 CACTCTGGAGACCGCGCGGATCCACAGGAGTCAACGGTTTCGGGAGGCGCGGATC 477  
Db 431 CAGCTCTGGAGACCGCGCGGATCCACAGGAGTCAACGGTTTCGGGAGGCGCGGATC 490  
QY 478 CAGGTATGATGAGCAGCGCGCGCTGGCGAGCTGCTGCTGCTCCACGCGCGGAG 537  
Db 491 CAGGTATGATGAGCAGCGCGCGCTGGCGAGCTGCTGCTGCTCCACGCGCGGAG 550  
QY 538 CCCAACTGGCGACAGCCTGCGCACTCTCACCCGACCGGTGATGCTGCTCCCGGAGGGC 597  
Db 551 CCCAACTGGCGACAGCCTGCGCACTCTCACCCGACCGGTGATGCTGCTCCCGGAGGGC 610  
QY 598 TTCCTGGACACGCTGTGTGCTGTGCTACCGGGCGGGCGGCTGGAGCTGCGCGATGCC 657

Db 611 TTCCTGGACACGCTGTGTGCTGTCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 670  
QY 658 TGGGTCGTCTGCCGCTGGACTTGGCCGAGGAGCGGGGCCACCGGAGCTTTCGAGGGTAC 717  
Db 671 TGGGTCGTCTGCCGCTGGACTTGGCCGAGGAGCGGGGCCACCGGAGCTTTCGAGGGTAC 730  
QY 718 CTGCGCACAGCCAGCGGGGAGTGCAGCCAGGTTCCCGAGCCGCCACACAGACTTTATTT 777  
Db 731 CTGCGCACAGCCAGCGGGGAGTGCAGCCAGGTTCCCGAGCCGCCACACAGACTTTATTT 790  
QY 778 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837  
Db 791 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 850  
RESULT 6  
US-08-474-177-15  
Sequence 15, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474.177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 335..751  
US-08-474-177-15

Query Match 80.9%; Score 677.2; DB 1; Length 751;  
Best Local Similarity 97.9%; Pred. No. 1.8e-143;  
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

Qy 1 GAGGACTCCGGGAGG-GTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 59  
Db 9 GAGGACTCCGGGAGGCTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 68  
Qy 60 GCGCTAGGCGCTTTTCCAGAACATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 119  
Db 69 GCGCTAGGCGCTTTTCCAGAACATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 128  
Qy 120 AAAAGCCGGAGCTAAGCAGCGCGCTCGG-CACTGACGGGCCCCAAGCCGAGAG 178  
Db 129 AAAAGCCGGAGCTAAGCAGCGCGCTCGGCACTGACGGGCCCCAAGCCG---AG 185  
Qy 179 AAGGACGAGCGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTGCGCC 238  
Db 186 AAGGACGAGCGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTGCGCC 245  
Qy 239 GGAGAGCGTGGGAAGGAAGAGAGTGTCTTAAGTTTACGGCCCAACGGTGGATTATC 298  
Db 246 GGAGAGCGTGGGAAGGAAGAGAGTGTCTTAAGTTTACGGCCCAACGGTGGATTATC 305  
Qy 299 CGGCGCTGCGCTCTGGGGCTGCGGAATGCGGAGGAGACAGGGGATGCCAGTG 358  
Db 306 CGGCGCTGCGCTCTGGGGCTGCGGAATGCGGAGGAGACAGGGGATGCCAGTG 365  
Qy 359 GGGCGGCGAGGATGAGGGTGTGGCCA---CGCGCGCGGGGAGTGTGAGGAAGGTGC 415  
Db 366 GGGCGGCGAGGATGAGGGTGTGGCCAAGCGCGCGCGGGGAGTGTGAGGAAGGTGC 425  
Qy 416 GACACTCTGGGAAGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGGCGGA 475  
Db 426 GACAGCTCTGGGAAGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGGCGGA 485  
Qy 476 TCCAGGTATCATGATGAGGAGCGCGCGTGGGAGGCTGCTGCTCCACGGCGCGG 535  
Db 486 TCCAGGTATCATGATGAGGAGCGCGCGTGGGAGGCTGCTGCTCCACGGCGCGG 545  
Qy 536 AGCCCACTGCGAGACCCCTGCCACTCTACCCAGCGGTGCATGATGCTGCCCGGGAGG 595  
Db 546 AGCCCACTGCGAGACCCCTGCCACTCTACCCAGCGGTGCATGATGCTGCCCGGGAGG 605  
Qy 596 GCTTCTGGACACGCTGGT 655  
Db 606 GCTTCTGGACACGCTGGT 665  
Qy 656 CTTGGGTGCTGCTGCGGTGACTTGGCGAGGAGCGGGCCACCGGACGTTGCAGGTT 715  
Db 666 CTTGGGTGCTGCTGCGGTGACTTGGCGAGGAGCGGGCCACCGGACGTTGCAGGTT 725  
Qy 716 ACCTGCGCACACCGCGGGGACTGA 741  
Db 726 ACCTGCGCACACCGCGGGGACTGA 751

## RESULT 7

us-08-487-033-15  
; Sequence 15, Application US/08487033  
; Patent No. 5739027  
; GENERAL INFORMATION:

APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1E1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 335..751  
US-08-487-033-15

Query Match 80.9%; Score 677.2; DB 2; Length 751;  
Best Local Similarity 97.9%; Pred. No. 1.8e-143;  
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

Qy 1 GAGGACTCCGGGAGG-GTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 59  
Db 9 GAGGACTCCGGGAGGCTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 68  
Qy 60 GCGCTAGGCGCTTTTCCAGAACATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 119  
Db 69 GCGCTAGGCGCTTTTCCAGAACATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 128





Qy	476	TCAGGTCATGATGATGGGAGCGCCCGGTGGCGGAGCTGCTGCTCCACGGCGGG	535
Db	486	TCCAGGTCATGATGATGGGAGCGCCCGGTGGCGGAGCTGCTGCTCCACGGCGGG	545
Qy	536	AGCCCAACTGCGAGACCCCTGCCACATCTACCCGACCGGTGCATGATGCTGCCGGAGG	595
Db	546	AGCCCAACTGCGAGACCCCTGCCACATCTACCCGACCGGTGCATGATGCTGCCGGAGG	605
Qy	596	GCTTCTCTGGACACGCTGGTGGTCTGCACCGGGCGGGCGCGGTGGACGTGCGCGATG	655
Db	606	GCTTCTCTGGACACGCTGGTGGTCTGCACCGGGCGGGCGCGGTGGACGTGCGCGATG	665
Qy	656	CTTGGGGTCGTCTGCCGTGGACTTGGCGAGAGAGCGGGCCACCGACGTTGCAGGCT	715
Db	666	CTTGGGGTCGTCTGCCGTGGACTTGGCGAGGAGCGGGCCACCGACGTTGCAGGCT	725
Qy	716	ACCTGGCGACAGCCAGGGGGACTGA	741
Db	726	ACCTGGCGACAGCCAGGGGGACTGA	751

RESULT 9  
 US-08-508-735-15  
 : Sequence 15, Application US/08508735  
 : Patent No. 5843756  
 : GENERAL INFORMATION:  
 : APPLICANT: Stone, Steven  
 : APPLICANT: Jiang, Ping  
 : APPLICANT: Kang, Alexander  
 : TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
 : NUMBER OF SEQUENCES: 47  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 : STREET: 1201 New York Avenue, Suite 1000  
 : CITY: Washington  
 : STATE: DC  
 : COUNTRY: USA  
 : ZIP: 20005  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/508,735  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US to be assigned  
 : FILING DATE: 07-JUN-1995  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/US95/03316  
 : FILING DATE: 17-MAR-1995  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Ihnen, Jeffrey L.  
 : REGISTRATION NUMBER: 28,957  
 : REFERENCE/DOCKET NUMBER: 24894-109348  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 202-962-4848  
 : TELEFAX: 202-962-8300  
 : INFORMATION FOR SEQ ID NO: 15:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 751 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : HYPOTHETICAL: NO  
 : ANTI-SENSE: NO  
 : ORIGINAL SOURCE:  
 : ORGANISM: Homo sapiens.  
 : FEATURE:



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 335..751  
US-08-486-047-15

Query Match 80.9%; Score 677.2; DB 4; Length 751;  
Best Local Similarity 97.9%; Pred. No. 1.8e-143;  
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

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DB 9 GAGGACTCGCGACGCGTCCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC 68  
QY 60 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCGCGCTGTTCTTGGAGCCGAGG 119  
DB 69 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCGCGCTGTTCTTGGAGCCGAGG 128  
QY 120 AAAGCCCGGAGCTACGACCGCGCGCTCGG-CAGTCGACGGGGCCCAAGCGCGAGAG 178  
DB 129 AAAGCCCGGAGCTAACGACCGCGCGCTCGGCACTGACGGGGCCCAAGCGCG--AG 185  
QY 179 AAGGACGACGGAGGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 238  
DB 186 AAGGACGACGGAGGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 245  
QY 239 GGAGCAGCTGGGAAAGAAAGGAGAGTGTCTTAAGTTTACGGCCACCGTGGATTATC 298  
DB 246 GGAGCAGCTGGGAAAGAAAGGAGAGTGTCTTAAGTTTACGGCCACCGTGGATTATC 305  
QY 299 CGGGCGCTGCGCTGCTGGGGCTCGGGAATGCGGAGGAGAGCAAGGATGCCAGTG 358  
DB 306 CGGGCGCTGCGCTGCTGGGGCTCGGGAATGCGGAGGAGAGCAAGGATGCCAGTG 365  
QY 359 GGGCGCGGACGATGAGGCTGTGGCA---CGCCGCGCGGGGAGTGTGGAGAGAGGTGC 415  
DB 366 GGGCGCGGACGATGAGGCTGTGGCA---CGCCGCGCGGGGAGTGTGGAGAGAGGTGC 425

QY 416 GACACTCTGGGAAGCCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGGA 475  
DB 426 GACAGCTCTGGGAAGCCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGGA 485  
QY 476 TCCAGGTGATGATGGGAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535  
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QY 716 ACCTGCGCACAGCCACGGGGGACTGA 741  
DB 726 ACCTGCGCACAGCCACGGGGGACTGA 751

RESULT 12  
US-09-120-130-15  
Sequence 15, Application US/09120130  
Patent No. 6037462  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: WTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,130  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/480,810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
US-09-120-130-15

Query Match      80.9%; Score 677.2; DB 5; Length 751;
Best Local Similarity 97.9%; Pred. No. 1.8e-143;
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

QY 1 GAGGACTCCGCGACG-GTCCGACACCTCGCGCAGAGCGGCTTGGAGCTCGGCTGCTTCC 59
Db 9 GAGGACTCCGCGACGCGTCCGACCTCGCGCAGAGCGGCTTGGAGCTCGGCTGCTTCC 68
QY 60 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCGCTGTTCTTGGAGCGCCAGG 119
Db 69 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCGCTGTTCTTGGAGCGCCAGG 128
QY 120 AAAGCCCGGAGCTACGACCGCGCGCTCGG-CACTGCACGGGCGCCCAAGCGCGAG 178
Db 129 AAAGCCCGGAGCTACGACCGCGCGCTCGGCACTGCACGGGCGCCCAAGCGCGC--AG 185
QY 179 AAGGACGACGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGGAGAGAGTGCGCC 238
Db 186 AAGGACGACGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGGAGAGAGTGCGCC 245
QY 239 GGAGCAGCGTGGGAAGAGGAAGAGTGTCTGTTAAGTTTACGGCCAAACGGTGGATTATC 298
Db 246 GGAGCAGCGTGGGAAGAGGAAGAGTGTCTGTTAAGTTTACGGCCAAACGGTGGATTATC 305
QY 299 CGGGCGCTGCGCGTCTGGGGCTGCGGAATGCGCGAGGAGACACAGGCGCATGCCAGTG 358
Db 306 CGGGCGCTGCGCGTCTGGGGCTGCGGAATGCGCGAGGAGACACAGGCGCATGCCAGTG 365
QY 359 GGGCGCGCAGCGATGAGGCTCTGGGCA---CGCCGCGCGGGGACTAGTGGAGAAGGTGC 415
Db 366 GGGCGCGCAGCGATGAGGCTCTGGGCAAGCGCGCGCGGGGACTAGTGGAGAAGGTGC 425
QY 416 GACACTCTGGGAAGCGCGCGGATGCCAAGAGTCAACCGTTTCGGGAGCGCGCGGA 475
Db 426 GACAGCTCTGGGAAGCGCGCGGATGCCAAGAGTCAACCGTTTCGGGAGCGCGCGGA 485
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Db 666 CTGCGGCTGCTGCTGCCCGTGGACTTGGCGAGGAGGCGCGCCACCGGACGTTGAGGTT 725
QY 716 ACCTGGCAGCAGCGACGGGGACTGA 741
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Db 726 ACCTGGCAGCAGCGACGGGGACTGA 751

RESULT 13
US-09-115-252-15
; Sequence 15, Application US/09115252
; Patent No 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,252
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
US-09-115-252-15
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Query Match 80.9%; Score 677.2; DB 5; Length 751;  
Best Local Similarity 97.9%; Pred. No. 1.8e-143;

Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

Qy 1 GAGGACTCCGGACG-GTCCGACCCCTGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTC 59  
Db 9 GAGGACTCCGGACGCGTCCGACCCCTGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTC 68  
Qy 60 GCGCTAGGCGCTTTTCCCAAGCAATCCAGGCGCGCCGCTGTTCTTGAGCGCCAGG 119  
Db 69 GCGCTAGGCGCTTTTCCCAAGCAATCCAGGCGCGCCGCTGTTCTTGAGCGCCAGG 128  
Qy 120 AAAGCCGCGAGCTAACGACCGCGCGCTCGG-CAGTGCACGGGGCCCAAGCCGAGAAG 178  
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Qy 179 AAGGACGACGGGAGGTTAATGAAGCTGAGCCCCAGGCTCTCTAGGAAGAGAGTGGGCC 238  
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Qy 239 GGAGCAGCGTGGGAAGAGAGAGTGTCTTAAGTTTACGGCCCAACGGTGTGATTATC 298  
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Qy 656 CTGGGGTCTGCTGCCGCTGGACTTGGCCGAGAGCGGGGCGCCAGCGTTCAGGGT 715  
Db 666 CTGGGGTCTGCTGCCGCTGGACTTGGCCGAGAGCGGGGCGCCAGCGTTCAGGGT 725  
Qy 716 ACCTGGCAGACGACGCGGGGACTGA 741  
Db 726 ACCTGGCAGACGACGCGGGGACTGA 751

RESULT 14  
US-08-474-177-5  
Sequence 5, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:

Query Match 43.0%; Score 360; DB 1; Length 1244;  
Best Local Similarity 100.0%; Pred. No. 1.7e-72;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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COMPUTER: IBM PC compatible  
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APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: intron  
LOCATION: 1..273  
FEATURE:  
NAME/KEY: misc\_RNA  
LOCATION: 274..529  
OTHER INFORMATION: /note= "Corresponds to exon of SEQ  
OTHER INFORMATION: ID NO:4"  
US-08-474-177-5







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GenCore version 4.5
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Perfect score: 837
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Searched:      5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 4	226.8	27.1	579	45	AI870879 w177d11.x
C 5	225.2	26.9	580	38	AI620409 qv39f07.x
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C 12	205.6	24.6	531	42	AI633790 t128e10.x
C 13	205.2	24.5	528	45	AI885362 w192h04.x
C 14	204.6	24.4	528	42	AI638416 t131g03.x
C 15	203.8	24.3	579	62	AW006218 w239g05.x
C 16	201	24.0	480	79	AW631047 hn91d11.y
C 17	194.8	22.3	546	21	AA085532 zn44e11.r
C 18	191.8	22.9	526	32	AA090181 o112b04.s
C 19	182.6	21.8	300	24	AA314567 EST186468
C 20	181.6	21.7	599	28	AA557137 n174b05.s
C 21	173.8	20.8	516	47	AI989792 w27c06.x
C 22	167.8	20.0	531	44	AI806771 w15a09.x
C 23	158	18.9	505	36	AI186333 qf30a08.x
C 24	157.8	18.9	496	71	AW328497 ds02h12.y
C 25	154.6	18.5	548	32	AA903110 ok52b03.s
C 26	149.6	17.9	533	32	AA877595 n107f06.s
C 27	147.8	17.7	494	69	AW190459 x115e01.x
C 28	142.8	17.1	531	33	AA946565 oq49e06.s
C 29	131.6	15.7	563	45	AI869175 w150c04.x
C 30	129.2	15.4	450	35	AI091727 ow59g04.x
C 31	117.4	14.0	689	38	AI373358 tb98f09.x
C 32	113.4	13.5	465	44	AI818660 w489c11.x
C 33	109.2	13.0	441	20	AA055664 w197f06.s
C 34	103.6	12.4	588	40	AI499733 tm91g12.x
C 35	103.2	12.3	606	44	AI798040 wh80g12.x
C 36	102.6	12.3	533	64	AW169901 x134d12.x
C 37	101.6	12.1	419	46	AI937552 wp78f11.x
C 38	101.4	12.1	510	39	AI401012 tg91f04.x
C 39	101.2	12.0	421	40	AI479957 tm73d10.x
C 40	100.6	12.0	550	37	AI245973 qk45h10.x
C 41	99.8	11.9	539	63	AW055075 wty99c10.x
C 42	99.6	11.9	557	42	AI656826 t154c09.x
C 43	99.4	11.9	537	36	AI221498 q867a12.x
C 44	99.4	11.9	597	43	AI703354 wq93c07.x
C 45	99.2	11.9	522	34	AI057178 oy78b02.x

## ALIGNMENTS

RESULT	1	EST	30-MAR-1999
LOCUS	AI394605/c	566 bp	IMAGE:2108696 3'
DEFINITION	cg13905.x1 NCI_CGAP_C111 Homo sapiens cDNA clone similar to SW:GDN2 HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR	mrna	INHIBITOR

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RESULT 2
AW328496      648 bp      mRNA      EST      28-JAN-2000
LOCUS      ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
DEFINITION      sequence.
ACCESSION      AW328496
VERSION      AW328496.1 GI:6798992
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 648)
AUTHORS      NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      On Apr 7, 1998 this sequence version replaced gi:3036295.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLCM0030 row: O column: 24
Seq primer: -21M13 forward primer (ABI).
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                /clone="IMAGE:2847599"
                /clone_lib="NIH_MGC_4"
                /cell_line="MGC1"
                /lab_host="DH10B"
                /note="Organ: Cervix; Vector: pORF7a; Site_1: ScaI;
                Site_2: CeuI; cDNA made by oligo-dT priming.
                Directionally cloned into CeuI/ScaI sites using the
                following 5' adaptor: taactatacggctcctaagtagcga and 3'
                adaptor: ttctacacctcttccgcacccacataaa. Average
                insert size 900 bp. Library prepared by Edge Biosystems."
BASE COUNT      127 a 200 c 196 g 123 t 2 others
ORIGIN
    Query Match      27.7%; Score 232; DB 71; Length 648;
    Best Local Similarity      81.7%; Pred. No. 9.1e-44;
    Matches 268; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 411 GGTGCGACACTCTCTGGGAAGCGCGCGGGATCCCAACGAGTCAACCGTTTCGGGAGCG 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 GCTGTGCCCTCTGCTGTGATGCTACTGAGGAGCAGCGTCTAGGCGAGCGCGCTTCCT 101
QY 471 CGCGATCCAGTCAATGATGGACAGCGCGCGGTGGCGAGCTGCTGCTGCCACGG 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 AGAAGACCAAGTCATGATGATGGCAGCGCGCGAGTGGCGAGCTGCTGCTCCACGG 161
QY 531 CGCGGACCCCAACTGCCAGACCTTGCACCTCTACCCGACCGGTGATGCTGCCCG 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 CGCGGAGCCCAACTGCGCCGACCCCGCACTCTCACCCGACCGGTGACGCGTGC 221
QY 591 GGAGGGCTTCTGTGACACGCTGTGTGCTGCACCGCGCGGGCGGGTGGACGTGCG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 GGAGGGCTTCTGTGACACGCTGTGTGCTGCACCGCGGGCGGGTGGACGTGCG 281
QY 651 CGATGCGCTGGGGTCTGTGCCCGGTGGACTTGGCGGAGAGCGGGCGCACGCGAGTGC 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 CGATGCGCTGGGGCGCTGTGCCCGGTGGACCTGTGCTGAGGAGCTGGGCCATCGCGATGTCG 341
QY 711 AGGTACTCTGGGCACACGCCACGGGGGAC 738
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Db 342 ACGGTACCTGCGCGGCTGCGGGGGC 369
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RESULT 3
AW328496      590 bp      mRNA      EST      07-MAR-2000
LOCUS      w18id11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3'
DEFINITION      similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
ACCESSION      AI871381
VERSION      AI871381.1 GI:5545430
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 590)
AUTHORS      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
JOURNAL      Disorders and Stroke, Brain Tumor Genome Anatomy Project
COMMENT      (CGAP/STGAP), Tumor Gene Index
Unpublished (1998)
On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 845 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 444.
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                /db_xref="taxon:9606"
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                /clone_lib="NCI_CGAP_Brn25"
                /tissue_type="anaplastic oligodendroglioma"
                /lab_host="DH10B"
                /note="Organ: brain; Vector: pTT3D-Pac (Pharmacia) with a
                modified Polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'
                TGTTCACATCTGAAGTGGGAGCGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
                T 3']; double-stranded cDNA was ligated to Eco RI
                adaptors (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of the modified pTT3 vector.
                Library is normalized, and was constructed by Bento
                Soares and M.Fatima Bonaldo."
BASE COUNT      114 a 158 c 179 g 139 t
ORIGIN
    Query Match      27.5%; Score 230; DB 45; Length 590;
    Best Local Similarity      92.4%; Pred. No. 2.6e-43;
    Matches 242; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 477 CCAGGTCAATGATGATGGCAGCGCGCGGTGGGAGCTGCTGCTCCACGCGCGGA 536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 CCAGGTCAATGATGATGGCAGCGCGCGAGAGTGGCGGAGCTGCTGCTCCACGCGCGGA 508
QY 537 GCCCAACTGCGAGACCTTGCCTCTCACCCGACCGGTGACATGCTGCCCGGGAGGG 596
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 507 GCCCAACTGCGGACCGCGCCACTCTCACCCGACCGGTGACATGCTGCCCGGGAGGG 448
QY 597 CTTCCTGGACACGCTGTGTGTGCTGCACCGGGCGGGCGCGGTGACGCTGCCGATGC 656
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7r3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 158 c 177 g 130 t 1 others.

ORIGIN

Query Match 26.9%; Score 225.2; DB 38; Length 580;  
Best Local Similarity 91.2%; Pred. No. 3.3e-42;  
Matches 239; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 477 CCAGGTCATGATGGGAGCGCCGCGTGGCGGAGCTGCTCTCCACGGCGCGGA 536  
DB 557 CCAGGTCATGATGGGAGCGCCGCGTGGCGGAGCTGCTCTCCACGGCGCGGA 498  
QY 537 GCCCAACTGGCAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGG 596  
DB 497 GCCCAACTGGCAGACTCCGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGG 438  
QY 597 CTTCTTGGACACGCTGGTGTGTGCACCGGGCGGGCGCGCTGGACGTGCGCGATGC 656  
DB 437 CTTCTTGAACACGCTGGTGTGTGCACCGGGCGGGCGCGCTGGACGTGCGCGATGC 378  
QY 657 CTGGGGTCTGCTCCGCTGGACTTGGCCGAGGAGCGGGCCACCGGACGTTGCAGGGTA 716  
DB 377 CTGGGGCTGCTCCGCTGGACTTGGCTGAGGAGCTGGGCCATCGCGATGTCGACGGTA 318  
QY 717 CTTGCGCACGCCACCGGGGAC 738  
DB 317 CTTGCGCGGCTGCGGGGGCG 296

RESULT 6  
AI198233/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI198233 579 bp mRNA EST 02-DEC-1998  
q155d12 x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3'  
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
; contains LTR9.b3 TARI TARI repetitive element ;, mRNA sequence.

AI198233  
AI198233.1 GI:3750839  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 579)  
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BrGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 729 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 459.  
Location/Qualifiers  
1. .579  
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/clone="IMAGE:1860407"  
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/lab\_host="DH10B"

FEATURES  
source

AI1765096 774 bp mRNA EST 21-DEC-1999  
wi48b08.x1 NCI\_CGAP\_Col16 Homo sapiens cDNA clone IMAGE:2393463 3'  
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains  
LTR9.b3 MER22 repetitive element ;, mRNA sequence.

AI1765096  
AI1765096.1 GI:5231605  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 774)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Feb 22, 1999 this sequence version replaced gi:4283180.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 854 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 400.  
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/organism="Homo sapiens"  
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/clone\_lib="NCI\_CGAP\_Col16"

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI1765096 774 bp mRNA EST 21-DEC-1999  
wi48b08.x1 NCI\_CGAP\_Col16 Homo sapiens cDNA clone IMAGE:2393463 3'  
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains  
LTR9.b3 MER22 repetitive element ;, mRNA sequence.

AI1765096  
AI1765096.1 GI:5231605  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 774)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Feb 22, 1999 this sequence version replaced gi:4283180.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 854 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 400.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/clone\_lib="NCI\_CGAP\_Col16"

FEATURES  
source



**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

**JOURNAL** Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

**MEDLINE** 99380589

**COMMENT** On Dec 15, 1999 this sequence version replaced gi:4575297.  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 651 row: K column: 23  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 614.  
Location/Qualifiers  
1. .614  
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/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"  
BASE COUNT 117 a 182 c 171 g 133 t 11 others  
ORIGIN

Query Match 26.2%; Score 219.2; DB 103; Length 614;  
Best Local Similarity 85.1%; Pred. No. 7.9e-41;  
Matches 245; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 478 CAGGTGATGATGGGACGCGCGGTGGCGAGCTGCTGTCTCCACGGCGGGAG 537  
Db 291 CAAGTCATGATGGGACCGCGGAGTGGCTGTCTCCACGGCGGGAG 350

QY 538 CCCAAGTGGCGAGACCTGCTCACTCTCACCCGAGTGGATGCTGCCCGGGAGGC 597  
Db 351 CCCAAGTGGCGAGACCTGCTCACTCTCACCCGAGTGGATGCTGCCCGGGAGGC 410

QY 598 TTCTTGACACGT 657  
Db 411 TTCTTGACACGT 470

QY 658 TGGGGT 717  
Db 471 TGGGGT 530

QY 718 CTGGGACACGACGGGGGACTGACGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 765  
Db 531 CTGGGCGGATGGGGGGACCATGATGATACCATGCTCCCGCATAGA 578

**RESULT** 10  
AI363262/c

**LOCUS** AI363262 708 bp mRNA EST 16-FEB-1999

**DEFINITION** qy56f03.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3' similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ; contains LTR.b3 TAR1 repetitive element ;, mRNA sequence.

**ACCESSION** AI363262  
VERSION AI363262.1 GI:4114883  
KEYWORDS EST.  
SOURCE human.

**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/dbbrp/image/image.html](http://www-bio.llnl.gov/dbbrp/image/image.html)  
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Seq primer: -40UP from Gibco  
High quality sequence stop: 394.  
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/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 137 a 210 c 219 g 140 t 2 others  
ORIGIN

Query Match 26.1%; Score 218.2; DB 38; Length 708;  
Best Local Similarity 79.0%; Pred. No. 1.4e-40;  
Matches 259; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 411 GGTGCACACTCTCTGGGAAGCGCGCGGATCCACGAGTCAACCGTTTCGGGAGCG 470  
Db 607 GCTGTGGCTTCTGCTGTGATGTACTGAGAAGCCACGCTCTAGGGCAGCAGCGCTTCT 548

QY 471 CGCGATCCAGGTATCATGATGGGACGCGCGGTGGCGAGCTGCTGCTCTCCACGG 530  
Db 547 AGAAGANAGGTATGATGTCAGCAAGCCCGAGTGGCAAGCTGCTGCTCTCCCGGG 488

QY 531 CGCGGAGCCCAACTGCGCAGACCTTCCCACTCTCACCCGACCGGTGATGATGCTCCCG 590  
Db 487 CGCGGAGCCCAACTGCGCAGACCTTCCCACTCTCACCCGACCGGTGATGATGCTCCCG 428

QY 591 GGAGGCTTCTTGGACACGCTGT 650  
Db 427 GGAGGCTTCTTGGACACGCTGT 368

QY 651 CGATGCTGGGTGCTGCTCCGTTGGACTTGGCCGAGGAGCGGGCCACCGGACCTTGC 710  
Db 367 CGATGCTGGGTGCTGCTCCGTTGGACTTGGCCGAGGAGCTGCTGAGGAGCTGGGCCATGCTCG 308

QY 711 AGGGTACCTGCGCACACGACCGGGGAC 738  
Db 307 ACGGTACCTGCGCGCGCTGCGGGGGC 280

**FEATURES**  
source

1. .708  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2016029"  
/clone\_lib="NCI\_CGAP\_Brn23"  
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/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 137 a 210 c 219 g 140 t 2 others  
ORIGIN

**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

**JOURNAL** Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

**MEDLINE** 99380589

**COMMENT** On Dec 15, 1999 this sequence version replaced gi:4575297.  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 651 row: K column: 23  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 614.  
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/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"  
BASE COUNT 117 a 182 c 171 g 133 t 11 others  
ORIGIN

Query Match 26.2%; Score 219.2; DB 103; Length 614;  
Best Local Similarity 85.1%; Pred. No. 7.9e-41;  
Matches 245; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 478 CAGGTGATGATGGGACGCGCGGTGGCGAGCTGCTGTCTCCACGGCGGGAG 537  
Db 291 CAAGTCATGATGGGACCGCGGAGTGGCTGTCTCCACGGCGGGAG 350

QY 538 CCCAAGTGGCGAGACCTGCTCACTCTCACCCGAGTGGATGCTGCCCGGGAGGC 597  
Db 351 CCCAAGTGGCGAGACCTGCTCACTCTCACCCGAGTGGATGCTGCCCGGGAGGC 410

QY 598 TTCTTGACACGT 657  
Db 411 TTCTTGACACGT 470

QY 658 TGGGGT 717  
Db 471 TGGGGT 530

QY 718 CTGGGACACGACGGGGGACTGACGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 765  
Db 531 CTGGGCGGATGGGGGGACCATGATGATACCATGCTCCCGCATAGA 578

**RESULT** 10  
AI363262/c

**LOCUS** AI363262 708 bp mRNA EST 16-FEB-1999

**DEFINITION** qy56f03.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3' similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ; contains LTR.b3 TAR1 repetitive element ;, mRNA sequence.

**ACCESSION** AI363262  
VERSION AI363262.1 GI:4114883  
KEYWORDS EST.  
SOURCE human.

**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/dbbrp/image/image.html](http://www-bio.llnl.gov/dbbrp/image/image.html)  
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High quality sequence stop: 394.  
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/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 137 a 210 c 219 g 140 t 2 others  
ORIGIN

Query Match 26.1%; Score 218.2; DB 38; Length 708;  
Best Local Similarity 79.0%; Pred. No. 1.4e-40;  
Matches 259; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 411 GGTGCACACTCTCTGGGAAGCGCGCGGATCCACGAGTCAACCGTTTCGGGAGCG 470  
Db 607 GCTGTGGCTTCTGCTGTGATGTACTGAGAAGCCACGCTCTAGGGCAGCAGCGCTTCT 548

QY 471 CGCGATCCAGGTATCATGATGGGACGCGCGGTGGCGAGCTGCTGCTCTCCACGG 530  
Db 547 AGAAGANAGGTATGATGTCAGCAAGCCCGAGTGGCAAGCTGCTGCTCTCCCGGG 488

QY 531 CGCGGAGCCCAACTGCGCAGACCTTCCCACTCTCACCCGACCGGTGATGATGCTCCCG 590  
Db 487 CGCGGAGCCCAACTGCGCAGACCTTCCCACTCTCACCCGACCGGTGATGATGCTCCCG 428

QY 591 GGAGGCTTCTTGGACACGCTGT 650  
Db 427 GGAGGCTTCTTGGACACGCTGT 368

QY 651 CGATGCTGGGTGCTGCTCCGTTGGACTTGGCCGAGGAGCGGGCCACCGGACCTTGC 710  
Db 367 CGATGCTGGGTGCTGCTCCGTTGGACTTGGCCGAGGAGCTGCTGAGGAGCTGGGCCATGCTCG 308

QY 711 AGGGTACCTGCGCACACGACCGGGGAC 738  
Db 307 ACGGTACCTGCGCGCGCTGCGGGGGC 280

**FEATURES**  
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/clone="IMAGE:2016029"  
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/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 137 a 210 c 219 g 140 t 2 others  
ORIGIN





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QY 622 CACCGGCGGGCGCGGTGGAGCTGCGCGATGCTCGTGGGGTGGTCTGCCCGTGACTTG 681
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Db 411 CACCGGCGGGCGCGGTGGAGCTGCGCGATGCTCGTGGGGTGGTCTGCCCGTGACTTG 352
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QY 682 GCGGAGGAGCGGGGCCACCGCGAGCTTGCAGGTGACCTGCGGCACACGCGGGGGAC 738
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 351 GCTGAGGAGCTGGGCCATCGCGATGCGCACGCTACCTGCGCGCGGTGCGGGGGC 295
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RESULT 13
AI885362/c 528 bp mRNA EST 07-MAR-2000
LOCUS w192h04.x1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432407 3'
DEFINITION similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A ; mRNA sequence.
ACCESSION AI885362
VERSION AI885362.1 GI:5590526
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project
(JCGRP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 626 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
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/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGGCGCGCGATAGTGTATTTTATTTTATTTT
TGTTCACATCTGAAGTGGGCGCGCGCGATAGTGTATTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 165 g 114 t
ORIGIN
Query Match 24.5%; Score 205.2; DB 45; Length 528;
Best Local Similarity 92.3%; Pred. No. 1.3e-37;
Matches 216; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 505 GTGCGGAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCAGACCTGCGACCTC 564
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Db 528 GTGCGGAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCAGACCTGCGACCTC 469
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QY 565 ACCGACCGGTGATGATGCTGCCCGGAGGGCTTCTCGACACGCTGGTGGCTGCAC 624
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Db 468 ACCGACCGGTGACACACGCTGCCCGGAGGGCTTCTCGACACGCTGGTGGCTGCAC 409
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QY 625 CGGGCGGGCGCGGTGGAGCTGCGCGATGCTCGTGGGGTGGTCTGCCCGTGACTTGCC 684
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Db 408 CGGGCGGGCGCGGTGGAGCTGCGCGATGCTCGTGGGGTGGTCTGCCCGTGACTTGCC 349
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QY 685 GAGGACGGGGCGCGACCGCGAGCTTGCAGGTGACCTGCGGCACACGCGGGGGAC 738
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Db 348 GAGGAGCTGGGCCATCGCGATGCTCGCACGCTACCTGCGCGCGGTGCGGGGGC 295
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RESULT 14
AI638416/c 528 bp mRNA EST 14-DEC-1999
LOCUS tt31g03.x1 NCI-CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
DEFINITION similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; contains LTR9.b3 TAR1 repetitive element ; mRNA sequence.
ACCESSION AI638416
VERSION AI638416.1 GI:4690650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40UP from Gibco
High quality sequence stop: 462.
FEATURES
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Location/Qualifiers
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/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI-CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 163 g 114 t
ORIGIN
Query Match 24.4%; Score 204.6; DB 42; Length 528;
Best Local Similarity 91.1%; Pred. No. 1.8e-37;
Matches 216; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 502 CGCGTGGCGAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCAGACCTGCGACT 561
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Db 528 CGAGTGGCGGAGCTGCTGCTCCTCACGGCGGAGCCCACTGCGNCGACNCCCCACT 469  
 QY 562 CTCACCCGACCGGTGCATGATGCTCCCGGGAGGCTTCCTGGACACGCTGCTGCTGCTG 621  
 Db 468 CTCACCCGACCGGTGCATGATGCTCCCGGGAGGCTTCCTGGACACGCTGCTGCTGCTG 409  
 QY 622 CACCGGGCGGGCGGGCTGACGTGCGGATGCGCTGGGGTCTGCTGCCCGTGGACTTG 681  
 Db 408 CACCGGGCGGGCGGGCTGACGTGCGGATGCGCTGGGGTCTGCTGCCCGTGGACTTG 349  
 QY 682 GCGGAGGAGCGGGCGGACCGCGGACGCTTGACGGGTACCTGCGCACAGCACGGGGGAC 738  
 Db 348 GCTGAGGAGCTGGGCCATGCGCATGCTGCACAGCTACTGCGGCGCGCTGCGGGGGGC 292

RESULT 15  
 LOCUS AW006218/c 579 bp mRNA EST 10-SEP-1999  
 DEFINITION w293905.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2566424 3',  
 similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
 ;, mRNA sequence.

ACCESSION AW006218  
 VERSION AW006218.1 GI:5854996  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 579)  
 NCBI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute / National Institute of Neurological  
 TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BTGP), Tumor Gene Index

JOURNAL Unpublished (1998)  
 COMMENT On Oct 6, 1998 this sequence version replaced gi:3705694.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 461.

FEATURES  
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 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAGTGGAGCGCGCCGATAGTGTGTTTTTTTTTTTTTTTTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT73 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 113 a 161 c 172 g 131 t 2 others  
 ORIGIN

Query Match 24.3%; Score 203.8; DB 62; Length 579;  
 Best Local Similarity 90.2%; Pred. No. 2.8e-37;  
 Matches 239; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

QY 474 GATCCAGTCAATGATGATGGGACAGCCCGCGGTGGCGAGCTGCTGCTGCTCCACGGCGC 533  
 Db 558 GACCAAGGTCAATGATGATGGGAGAGCGCCCGAG-GGCGAGCTGCTGCTGCTCCACGGG 500  
 QY 534 GGAGCCCAACTGGCGACAGACCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGA 593  
 Db 499 GGAGCCCAANTGCGCGGACCC-GCCACTCTCACCCGACCGGTGCACAGCTGCCCGGGA 441  
 QY 594 GGGCTTCTTGACACACGCTGGTGGTGGTGCACCGGGCGGGCGGGTGGACGTGCGCGA 653  
 Db 440 GGGCTTCTTGACACACGCTGGTGGTGGTGCACCGGGCGGGCGGGTGGACGTGCGCGA 381  
 QY 554 TGCTTGGGGTCTGCTGCCCGTGGACTTGGCGGAGAGCGGGGGCCACCGCGACGTTCAGG 713  
 Db 380 TGCTTGGGGCGGCTGCTGCCCGTGGACTTGGAGAGCTGGGCGCATCGCGATGTCGACG 321  
 QY 714 GTACCTGGGCACACGCCACGGGGGAC 738  
 Db 320 GTACCTGGCGCGGCTGCGGGGGGC 296

Search completed: July 21, 2000, 02:48:45  
 Job time: 9640 sec

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Date: Jul 21, 2000 8:05 AM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500  
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-LONGLOG -NO\_XLPXY -WAIT -THREADS=1

Search information block:  
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Query length: 137  
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Search time (sec): 1513.910000

score\_list:

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gb_pr3:HSU17075	+	667.50	915.46	6.8e-43	738	U17075 Human p14-CDK inhibitor
gb_pat:AR001326	+	667.50	915.34	6.9e-43	751	AR001326 Sequence 15 from patent
gb_pat:AR037506	+	667.50	915.34	6.9e-43	751	AR037506 Sequence 15 from patent
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gb_pat:I41160	+	667.50	915.34	6.9e-43	751	I41160 Sequence 15 from patent
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gb_pr3:S79760	+	555.00	762.46	2.3e-34	706	S79760 In4 rats, kidney, mRNA
gb_ro:AF059567	+	550.00	751.48	9.2e-34	1301	AF059567 Mus musculus cyclin d
gb_pat:AR062815	+	545.50	753.51	7.1e-34	393	AR062815 Sequence 45 from patent
gb_pat:AR001314	+	506.50	699.13	7.6e-31	471	AR001314 Sequence 1 from patent
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gb_pat:AR062774	+	506.50	699.13	7.6e-31	471	AR062774 Sequence 1 from patent
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gb_pat:AR001346	+	506.50	694.37	1.4e-30	947	AR001346 Sequence 36 from patent
gb_pat:AR037526	+	506.50	694.37	1.4e-30	947	AR037526 Sequence 36 from patent
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gb_pat:I41180	+	506.50	694.37	1.4e-30	947	I41180 Sequence 36 from patent
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gb_pat:I67718	+	496.50	677.98	1.1e-29	1420	I67718 Sequence 1 from patent
gb_pr4:S69805	+	451.00	623.71	1.2e-26	457	S69805 MTS2-multiple tumor sup
gb_pat:AR001317	+	451.00	616.88	2.9e-26	1244	AR001317 Sequence 5 from patent
gb_pat:AR037497	+	451.00	616.88	2.9e-26	1244	AR037497 Sequence 5 from patent
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gb_pat:I41151	+	451.00	616.88	2.9e-26	1244	I41151 Sequence 5 from patent
gb_pr4:AF000049	+	451.00	592.54	3.6e-25	44160	AF000049 Homo sapiens Chromos
gb_pr4:AF115544	+	434.00	596.79	3.8e-25	793	AF115544 Homo sapiens cyclin-d
em_om:AB010808	+	430.00	591.79	7.2e-25	742	AB010808 Felis catus gene for p
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gb_pr2:HSU26727	+	423.00	580.10	3.2e-24	1017	U26727 Human p16INK4/MTS1 mRNA
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gb_pat:AR062785	+	423.00	579.38	3.6e-24	1131	AR062785 Sequence 13 from pat
gb_pat:I41159	+	423.00	579.38	3.6e-24	1131	I41159 Sequence 13 from patent
gb_pr4:S69804	+	420.00	581.47	2.7e-24	457	S69804 MTS1-multiple tumor sup
gb_pr3:S698251	+	420.00	580.33	3.2e-24	540	S69822 Homo sapiens CDK41 exon,
gb_pr3:HSPCDK2	+	420.00	579.79	3.4e-24	585	U12819 Human p16-INK4 (p16) gen
gb_pat:AR001316	+	420.00	574.96	6.3e-24	1187	AR001316 Sequence 4 from patent
gb_pat:AR037496	+	420.00	574.96	6.3e-24	1187	AR037496 Sequence 4 from patent
gb_pat:AR062776	+	420.00	574.96	6.3e-24	1187	AR062776 Sequence 4 from patent
gb_pat:I41150	+	420.00	574.96	6.3e-24	1187	I41150 Sequence 4 from patent

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seq\_name: gb\_pr1:HUMCIP  
seq\_documentation\_block:  
LOCUS HUMCIP 837 bp mRNA PRI 08-OCT-1994  
DEFINITION Homo sapiens (clone p15INK4B/HAS) CDK inhibitory protein mRNA,  
complete cds.  
ACCESSION L36844  
VERSION L36844.1 GI:5561197  
KEYWORDS CDK inhibitory protein.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 837)  
AUTHORS Hannon,G.J. and Beach,D.  
TITLE p15INK4B is a potential effector of TGF-beta induced cell cycle  
arrest  
JOURNAL Nature 371, 257-261 (1994)  
MEDLINE 94359613  
FEATURES  
Location/Qualifiers  
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CDS 328..741  
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3'UTR 152 a 258 c 304 g 123 t  
BASE COUNT 152 a 258 c 304 g 123 t  
ORIGIN  
alignment\_scores:  
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17 yLeuAlaThrProAlaArgGlyLeuValGluLysValArgHisSerTrpG 34  
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378 TCTGCCACCGCGCGGGGACCTAGTGGAGAAAGTGGACACCTCTGGG 427  
34 luAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAlaAlaile 50  
|||||  
428 AGCGCGCGCGGATCCCAACGAGATCAACCGTTTCGGGAGCGCGCGATC 477  
51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH 67  
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478 CAGGTGATGATGATGGGCGAGCGCGCGTGGCGAGCTGCTGCTCCA 527  
67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84

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528 CGCGGGAGCCCAACTGCGACACCTGCACTCTCACCCGACCGGTGC 577
84 isAspAlaAaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
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578 ATGATGCTGCCCGGGAGGGCTTCTTGACACGCTGGTGTCTGCACCGG 627
101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 117
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628 GCCGGGGCGGGCTGGAGCGTCCGATGCTGGGGTCTGTCGCCGTGGA 677
117 pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThra 134
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678 CTTGGCGGAGGCGGGGCCACCGACGTGACGGGTACCTGCGCACAG 727
134 laThrGlyAsp 137
728 CCACGGGGGAC 738
seq_name: gb_pr3:HSU17075
seq_documentation_block:
LOCUS HSU17075 738 bp mRNA PRI 27-JAN-1995
DEFINITION Human p14-CDK inhibitor mRNA, complete cds.
ACCESSION U17075
VERSION U17075.1 GI:639715
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 738)
Guan,K.L., Jenkins,C.W., Li,Y., Nichols,M.A., Wu,X., O'Keefe,C.L.,
Matera,A.G. and Xiong,Y.
Growth suppression by p18, a p16INK4/MTS1- and
p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb
function
JOURNAL Genes Dev. 8 (24), 2939-2952 (1994)
MEDLINE 95095079
REFERENCE 2 (bases 1 to 738)
AUTHORS Guan,K.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1994) Kun-Liang Guan, Biological Chemistry,
University of Michigan, 1301 East Catherine, Ann Arbor, MI 48109,
USA
FEATURES
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322..738
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33 rGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
|||||
422 TGAAGCCGCGCGGATCCCAACGAGGTCAACCGTTTCGGGAGGCGCG 471
50 ileGlnValMetMetMetClySerAlaArgValAlaGluLeuLeuLeu 66
|||||
472 ATCCAGGTGATGATGGCAGCGCCCGCGGGAGGCTGCTGCTGCT 521
66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
|||||
522 CCACGGCGGAGCCCAACTGCGCAGACCTGCTCACTCTCACCCGACCGG 571
83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
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572 TGCATGATGCTCCCGGGAGGGCTTCTTGACACGCTGGTGTGCTGCAC 621
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
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622 CGGGCGGGGCGGCTGGACGTGCGATGCTGGGTGCTGCTGCCGT 671
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672 GCAGTTGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGTACTGTGCGCA 721
133 hrAlaThrGlyAsp 137
722 CAGCCACGGGGGAC 735
seq_name: gb_pat:AR001326
seq_documentation_block:
LOCUS AR001326 751 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 15 from patent US 5739027.
ACCESSION AR001326
VERSION AR001326.1 GI:3963393
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 751)
AUTHORS Kamb,A.
TITLE MTS1E1.beta. gene
JOURNAL Patent: US 5739027-A 15 14-APR-1998;
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385 TCTGGCCAGCGCGCGGGGACTAGTGGAGAGGTGCGACAGCTCC 434

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50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
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635 CGGCGCGCGCGGCTGGACGTGCGCGATGCTGGGGTCTGCTGCCCGT 684
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seq\_name: gb\_pat:AR037506

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LOCUS AR037506 751 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 15 from patent US 5801236.  
ACCESSION AR037506  
VERSION AR037506.1 GI:5955362  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 751)  
AUTHORS Kamb, A.  
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes  
JOURNAL Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes  
PATENT: US 5801236-A 15 01-SEP-1998;  
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Location/Qualifiers  
source  
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alignment\_scores:  
Quality: 667.50 Length: 138  
Ratio: 4.981 Gaps: 1  
Percent Similarity: 97.101 Percent Identity: 95.652

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US-09-016-869A-4 x AR037506 ..

Align seg 1/1 to: AR037506 from: 1 to: 751

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seq\_name: gb\_pat:AR062786

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LOCUS AR062786 751 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 15 from patent US 5843756.  
ACCESSION AR062786  
VERSION AR062786.1 GI:5990477  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 751)  
AUTHORS Stone, S., Jiang, P. and Kamb, A.  
TITLE Mouse MTS1 gene  
JOURNAL Mouse MTS1 gene  
PATENT: US 5843756-A 15 01-DEC-1998;  
FEATURES  
Location/Qualifiers  
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Percent Similarity: 97.101 Percent Identity: 95.652

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US-09-016-869A-4 x AR062786 ..

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385 TCTGGCCAGCGCGCGGCGGACTAGTGGAGAGGTGCGACAGCTCC 434
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66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 83
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LOCUS I41160 751 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 15 from patent US 5624819.
ACCESSION I41160
VERSION I41160.1 GI:2081750
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 751)
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Germ-line mutations in the MTS gene
JOURNAL Patent: US 5624819-A 15 29-APR-1997;
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66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 83
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116 laspleuAlaGluArgGlyHisArgaspValAlaGlyTyrLeuArgT 133
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735 CAGCCACGGGGGAC 748
seq_name: gb_pr3:AF004819
seq_documentation_block:
LOCUS AF004819 859 bp mRNA PRI 11-SEP-1997
DEFINITION Homo sapiens alternative spliced form of p15 CDK inhibitor mRNA,
complete cds.
ACCESSION AF004819
VERSION AF004819.1 GI:2257934
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS Tsubari,M., Tiitonen,E. and Laiho,M.
TITLE Cloning and characterization of p10, an alternatively spliced form
of p15 cyclin-dependent kinase inhibitor
JOURNAL Cancer Res. 57 (14), 2966-2973 (1997)
MEDLINE 97373727
REFERENCE 2 (bases 1 to 859)
AUTHORS Tsubari,M., Tiitonen,E. and Laiho,M.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-1997) Department of Virology, Haartman Institute,
University of Helsinki, P.O. Box 21, Helsinki 00014, Finland
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50 Ilegln.....
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52 .....ValMetMetGlySerAla 58
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570 ATTGTACAGAGTCTCGTTGGCGGAGGTCATGATGGCAGCGCC 619
59 ArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAs 75
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620 CGCGTGGCGAGCTGCTGCTCCACGCGGAGCCCACTGCGCAGA 669
75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 92
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670 CCCTGCCACTCTCACCGACCGGTGCATGATGCTGCCGCGGAGGCTTCC 719
92 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 108
|||||
720 TGGACAGCTGGTGTCTGCACCGCGCGGCGCGGCTGAGTGGCGC 769
109 AspAlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisAr 125
|||||
770 GATGCTGGGTCGCTGCTGCCGCTGGACTGGCGGAGGCGGCGCACCG 819
125 gAspValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
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ACCESSION S79760
VERSION S79760.1 GI:1176432
KEYWORDS
SOURCE Rattus sp. kidney.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 706)
Tsuchiya,H., Kikuchi,Y. and Mitani,H.
Hino,O., Kobayashi,E., Hirayama,Y., Kobayashi,T., Kubo,Y.,
Molecular genetic basis of renal carcinogenesis in the Eker rat
model of tuberous sclerosis (Tsc2)
JOURNAL Mol. Carcinog. 14 (1), 23-27 (1995)
MEDLINE 96001392
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 171930] from the original journal article.
Map location: 5q.
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BASE COUNT 142 a 212 c 231 g 121 t  
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alignment\_block:

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Align seg 1/1 to: S79760 from: 1 to: 706

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18 uAlaThr....ProAlaArgGlyLeuValGluLysValArgHisSerTrpG 34
|||||
190 GGCACCGCGCGCGCGGAGCAGGTGGAGACGGTGGCGCAGCTCCTGG 239
34 luAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAlaAla 50
|||||
240 AAGCGGCGCAGATCCCAACGCCGTCAACCGCTTCGGGAGGCGGCCGATC 289
51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH 67
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290 CAGGTCAATGATGATGGGCGGCGCGCGGCGGCGGCGGCGGCGGCGG 339
67 sGlyValAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
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340 CGGAGCAGAACCCCACTGCCCGCATCTGCCACCTCACCAGACCTGTGC 389
84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
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390 ATGATGAGCTCGAGAGGGCTTCTGGACAGGCTAATGGTGTGCACAAG 439
101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
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440 GCAGGGCAGCGGCTGTGTGTGACGCGCTGGCGCGCGCTGCGCGGTAGA 489
117 pLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgThra 134
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490 CTTAGCTGAAGACGAGCGGCCACCGTATATTGGCAGGTATCTGCACGCTG 539
134 laThrGlyAsp 137
|||||
540 CCACCTGGAGAT 550

seq_name: gb_ro:AF059567

seq_documentation_block: 1301 bp mRNA ROD 22-APR-1998
LOCUS AF059567
DEFINITION Mus musculus cyclin dependent kinase inhibitor 2B (Cdkn2b) mRNA,
complete cds.
ACCESSION AF059567
VERSION AF059567.1 GI:3075496
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1301)
Quelle,D.E., Ashmun,R.A., Hannon,G.J., Rehberger,P.A., Trono,D.,
Richter,K.H., Walker,C., Beach,D., Sherr,C.J. and Serrano,M.
Cloning and characterization of murine p16INK4a and p15INK4b genes
JOURNAL Oncogene 11 (4), 635-645 (1995)
MEDLINE 95380169
REFERENCE 2 (bases 1 to 1301)
AUTHORS Quelle,D.E., Ashmun,R.A., Hannon,G.J., Rehberger,P.A., Trono,D.,
Richter,K.H., Walker,C., Beach,D., Sherr,C.J. and Serrano,M.
Direct Submission
```

JOURNAL Submitted (14-APR-1998) Immunology and Oncology, National Center of  
Biotechnology, Campus de Cantoblanco, Madrid E-28049, Spain

## FEATURES

source  
1. .1301  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/chromosome="4"  
/map="C3-C6"  
/cell\_line="p19"  
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1. .1301  
/gene="Cdkn2b"  
145. .537  
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/note="p15INK4b; CDKN2B"  
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/translation="MLGSSDAGLATAAARGQVETVROLLEAGADPNALNRFGRRIQ  
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BASE COUNT 322 a 347 c 361 g 271 t  
ORIGIN

alignment\_scores:  
Quality: 550.00 Length: 134  
Ratio: 4.508 Gaps: 2  
Percent Similarity: 91.045 Percent Identity: 83.582

## alignment\_block:

US-09-016-869A-4 x AF059567 ..

Align seg 1/1 to: AF059567 from: 1 to: 1301

5 AsnLysGlyMetProSerGlyGlySerAspGluGlyLeuAlaThr... 20  
136 GACAGGGGATG...TTGGCGCGGACGATGACGGCGCTGGCCACCGC 182  
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37  
183 CGCGGGCGGGGCAAGTGGAGACGGTGGCGGAGCTCTGGAGCGGGG 232  
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53  
233 CAGATCCCAACGCCCTGAACCGCTTCGGAGGCGGCCAATCCAGGTCTATG 282  
54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyValAcl 70  
283 ATGATGGGCGGCGCCAGTGGCGAGAGCTGCTGCTCCACGGAGCAGA 332  
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87  
333 ACCCAACTGGCGGACCTGCCACCTTACCAGACCTGTGTCAGCGCAG 382  
87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103  
383 CTCGGGAGGCTCTCGACACGGCTTGTGCTGCACCGGGCGGGGG 432  
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaCl 120  
433 CGGTGGATGTGTGTGACCGCTGGGCGCCCTGGCGGTAGCTTGGCTGA 482  
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGlyA 137  
483 AGAGCAGGGCCCGCTGACATTCGAGGATCTTGCACGCTGCCACTGGAG 532  
137 sp 137  
533 AT 534

seq\_name: gb\_pat:AR062815

## seq\_documentation\_block:

LOCUS AR062815 393 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 45 from patent US 5843756.  
ACCESSION AR062815  
VERSION AR062815.1 GI:5990506  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 393)  
AUTHORS Stone,S., Jiang,P. and Kamb,A.  
TITLE Mouse MTSI gene  
JOURNAL Patent: US 5843756-A 45 01-DEC-1998;  
FEATURES Location/Qualifiers  
1. .393  
source  
BASE COUNT 69 a 124 c 141 g 59 t  
ORIGIN

alignment\_scores:  
Quality: 545.50 Length: 128  
Ratio: 4.623 Gaps: 1  
Percent Similarity: 92.188 Percent Identity: 85.156

## alignment\_block:

US-09-016-869A-4 x AR062815 ..

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11 GlyGlyGlySerAspGluGlyLeuAlaThr...ProAlaArgGlyLeuVa 26  
7 GCGGCGACGAGTGGCGGCTGGCCACCGCGCGCGCGGCGGCAAGT 56  
26 lclLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyValA 43  
57 GGAGACGGTGGCGCAACTCTGGAAGCGCGGCGAGATCCCAACGCCCTGA 106  
43 snArgPheGlyArgAlaIleGlnValMetMetMetGlySerAlaArg 59  
107 ACCGCTTCGGAGGGCGCCCAATCCAGGTTCATGATGGCGAGCGCCAG 156  
60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76  
157 GTGGCAGAGCTGCTGCTGCTCCAGGAGCAGAACCAACTGCGCGACCC 206  
76 cAlaThrLeuThrArgProValHisAspAlaArgGluGlyPheLeuA 93  
207 TGCCACCTTACCAGACCTGTGCAGCGAGCTCGGAAGGCTTCCTGG 256  
93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109  
257 ACACGCTTGTGCTGCTGCACCGCGGCGCGGCTGATGTGTGTGAC 306  
110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126  
307 GCCTGGGCGCGCTGCGGTAGACTTGGCTGAAGAGCAGGAGCCACCGTGA 356  
126 pValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137  
357 CATTCGAGGATCTGACGCTGCCACTGGAGAT 390  
seq\_name: gb\_pat:AR001314

## seq\_documentation\_block:

LOCUS AR001314 471 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 1 from patent US 5739027.  
ACCESSION AR001314  
VERSION AR001314.1 GI:3963381  
KEYWORDS  
SOURCE Unknown.





## alignment\_block:

US-09-016-869A-4 x AR062774

Align seg 1/1 to: AR062774 from: 1 to: 471

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 CCGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGGC 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57 CCGCGCGCGGGGTCGGGTACGAGAGGTGCGGCGCTGCTGGAGCGGGG 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
107 CGTGTGCCAACGACCGAATAGTTACGCTGGAGCGGATCCAGGTCATG 156
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 ATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCACGCGCGGA 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAla 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
207 GCCCAACTGCGCGACCCCGCACTCTCACCACCGCGTGCACGCGCTG 256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CCCGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGCGCGGGCG 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAla 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
207 GCCCAACTGCGCGACCCCGCACTCTCACCACCGCGTGCACGCGCTG 256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CCCGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGCGCGGGCG 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
307 CGGCTGACGTGGCGATGCTGGGGCGGCTGCTGCCGTGGACCTGGCTGA 356
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 GGAGCTGGGCATCGCATGTCGACGCTGCTGCTGACCGCGCGGCTGCGGG 405
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
307 CGGCTGACGTGGCGATGCTGGGGCGGCTGCTGCCGTGGACCTGGCTGA 356
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 GGAGCTGGGCATCGCATGTCGACGCTGCTGCTGACCGCGCGGCTGCGGG 405
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seq\_name: gb\_pat:I41148

## seq\_documentation\_block:

LOCUS I41148 471 bp DNA PAT 13-MAY-1997

DEFINITION Sequence 1 from patent US'5624819.

ACCESSION I41148

VERSION I41148.1 GI:2081738

## KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 471)

AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.

TITLE Germline mutations in the MTS gene

JOURNAL Patent: US 5624819-A 1 29-APR-1997;

FEATURES

Location/Qualifiers

1..471

/organism="unknown"

BASE COUNT 68 a 153 c 186 g 64 t

## ORIGIN

## alignment\_scores:

Quality: 506.50 Length: 133

Ratio: 4.404 Gaps: 2

Percent Similarity: 86.466 Percent Identity: 80.451

## alignment\_block:

US-09-016-869A-4 x I41148

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7 CCGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGGC 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
|||||
157 ATGATGGGACGCGCCAGTGGCGAGCTGCTGTCTCCACGGCGCGGA 206
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
|||||
207 GCCCAACTGGCGCGACCCGCCACTCTCACCCGACCGGTGCACGACGCTG 256
87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
|||||
257 CCCGGAGGGCTTCCTGGACACGCTGGTGTCTGCACCGCGCGGGGCG 306
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGl 120
|||||
307 CGGCTGGACGTGCCGATGCCCTGGGGCGCTCTGCCGTGGACCTGGGCTGA 356
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
|||||
357 GGAGCTGGGCCATCGCGATGTCGCACGGTACCTCGCGCGCGGCTCGGGGG 405
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OM of: US-09-016-869a-4 to: N\_Geneseq\_36.\* out\_format : pfs

Date: Jul 21, 2000 9:30 AM

About: Results were produced by the GenCore software, version 4.5.

Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
 -MODEL=frame+p2n.model -DEV=xlp  
 -O=/cgn2.1/USPTO\_spool/US09016869/runat\_20072000\_083607\_16111/app\_query.fasta\_1.598  
 -DB=N\_Geneseq\_36 -OPT=fastap -SUFFIX=ring -GAPOP=12.000  
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
 -GAPOP=4.500 -GAPEXT=0.050 -GAPOP=10.000 -XGAPEXT=0.500  
 -GAPOP=6.000 -GAPEXT=7.000 -GAPOP=10.000 -XGAPEXT=0.500  
 -DELOP=6.000 -DELOP=7.000 -START=1 -MATRIX=blotsum62  
 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR\_SCORE=pet  
 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
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Search information block:

Query: US-09-016-869A-4

Query length: 137

Database: N\_Geneseq\_36.\*

Database sequences: 311585

Database length: 125056042

Search time (sec): 109.050000

score\_list:

Sequence	Strd	Orig	Zscore	EScore	Len	Documentation
N_Geneseq_36:T00745	+	667.50	1163.10	3.5e-57	751	Multiple tumour suppressor 2 (M
N_Geneseq_36:Q99165	+	667.50	1163.10	3.5e-57	751	Human multiple tumour suppressor
N_Geneseq_36:T69781	+	667.50	1163.10	3.5e-57	751	Human multiple tumour suppressor
N_Geneseq_36:V11250	+	667.50	1163.10	3.5e-57	751	Human MTS2 cDNA. DNA specific f
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N_Geneseq_36:V70595	+	667.50	1163.10	3.5e-57	751	CNA encoding a human multiple
N_Geneseq_36:T02963	+	659.50	1147.98	2.4e-56	850	Cell-cycle regulatory protein p
N_Geneseq_36:T02964	+	554.00	966.44	3.1e-46	580	Cell-cycle regulatory protein p
N_Geneseq_36:V70624	+	545.50	954.98	1.4e-45	393	Mouse multiple tumour suppressor
N_Geneseq_36:T26232	+	513.00	889.13	6.3e-42	1073	Truncated p27/p16 fusion protei
N_Geneseq_36:X26234	+	509.00	884.92	1.1e-41	782	Truncated p27/p16 fusion protei
N_Geneseq_36:V11238	+	506.50	885.02	1.1e-41	471	Human MTS1 cDNA. DNA specific f
N_Geneseq_36:V70583	+	506.50	885.02	1.1e-41	471	Nucleotide sequence of the CDS
N_Geneseq_36:V70583	+	506.50	885.02	1.1e-41	471	CNA encoding a human multiple
N_Geneseq_36:T26233	+	506.50	881.06	1.8e-41	737	Truncated p27/p16 fusion protei
N_Geneseq_36:T72311	+	506.50	878.84	2.4e-41	947	Human multiple tumour suppressor
N_Geneseq_36:V11270	+	506.50	878.84	2.4e-41	947	Human MTS1 cDNA variant. DNA sp
N_Geneseq_36:V53851	+	506.50	878.84	2.4e-41	947	Coding sequence 3 of the multipe
N_Geneseq_36:V70615	+	506.50	878.84	2.4e-41	947	CNA encoding a human multiple
N_Geneseq_36:T60951	+	506.50	878.47	2.5e-41	987	Tumour suppressor p16 coding se
N_Geneseq_36:X26231	+	506.50	878.11	2.6e-41	1028	Truncated p27/p16 fusion protei
N_Geneseq_36:T74053	+	506.50	877.53	2.8e-41	1098	CDK inhibitory fusion protein
N_Geneseq_36:X26224	+	506.50	877.53	2.8e-41	1098	Human p16p27 fusion protein en
N_Geneseq_36:X26235	+	506.50	877.35	2.9e-41	1121	Human p16p27 fusion protein en
N_Geneseq_36:T74052	+	506.50	877.17	2.9e-41	1143	CDK inhibitory fusion protein
N_Geneseq_36:X26231	+	506.50	877.17	2.9e-41	1143	Human p16(GS)p27 fusion protei
N_Geneseq_36:T69768	+	499.50	872.75	5.2e-41	471	Human multiple tumour suppressor
N_Geneseq_36:T69769	+	498.50	871.00	6.5e-41	471	Human multiple tumour suppressor
N_Geneseq_36:T00747	+	497.50	863.06	1.8e-40	947	Multiple tumour suppressor 1 (M
N_Geneseq_36:T02962	+	496.50	862.64	1.9e-40	994	Cell-cycle regulatory protein p
N_Geneseq_36:T74051	+	496.50	857.73	3.6e-40	1420	CDK inhibitory fusion protein
N_Geneseq_36:X26220	+	496.50	857.73	3.6e-40	1420	Human p27-p16 fusion protein e
N_Geneseq_36:T00736	+	493.50	862.70	1.9e-40	447	Multiple tumour suppressor 1 (M
N_Geneseq_36:T093158	+	493.50	862.70	1.9e-40	447	Human multiple tumour suppressor
N_Geneseq_36:T063491	+	493.50	856.04	4.4e-40	948	Inhibitor of cyclin dependent k
N_Geneseq_36:T00749	+	486.50	850.43	9.1e-40	447	Multiple tumour suppressor 1 (M
N_Geneseq_36:T00750	+	485.50	848.67	1.1e-39	447	Multiple tumour suppressor 1 (M
N_Geneseq_36:T00741	+	451.00	779.14	8.5e-36	1244	Human MTS2 DNA including exon
N_Geneseq_36:Q99168	+	451.00	779.14	8.5e-36	1244	Human MTS2 genomic DNA includi
N_Geneseq_36:V11241	+	451.00	779.14	8.5e-36	1244	Nucleotide sequence of the mul

N\_Geneseq\_36:V70586 + 451.00 779.14 8.5e-36 1244 Human multiple tumour suppressor  
 N\_Geneseq\_36:T00744 + 423.00 730.91 4.1e-33 1131 Multiple tumour suppressor  
 N\_Geneseq\_36:Q99164 + 423.00 730.91 4.1e-33 1131 Human MTS polypeptide, MTS1  
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seq\_name: N\_Geneseq\_36:T00745

seq\_documentation\_block:

ID T00745 standard; CDNA; 751 BP.

AC T00745;

DT 08-MAY-1996 (first entry)

DE Multiple tumour suppressor 2 (MTS2) gene ORF.

KW Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;

KW predisposition; melanoma; leukaemia; lymphoma; prognosis;

OS pancreas; breast; thyroid; open reading frame; ORF; ds.

OS Homo sapiens.

FH Key

FT cds

FT cds

PN WO9525813-A1.

PD 28-SEP-1995.

PF 17-MAR-1995; U03537.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215087.

PR 18-MAR-1994; US-215086.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PA (MYRI-) MYRIAD GENETICS INC.

PI (UTAH) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

DR WPI: 95-344626/44.

DR P-PSDB; R81702.

PT Detecting polymorphism associated with cancer pre:disposition - also

PT DNA, vectors and host cells e.g. for gene or protein replacement

PT therapy and drug screening

PS Disclosure: Pages 102-103; 148pp; English.

CC An individual can be diagnosed as having a predisposition to cancer

CC by detecting an alteration in the wild type multiple tumour

CC suppressor (MTS) gene, using gene probes which hybridise to the MTS2

CC gene ORF T00745 (which encodes R81702). The above assay can also be

CC used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia

CC and pancreas, breast and thyroid cancers, etc.

SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment\_scores:

Quality: 667.50 Length: 138

Ratio: 4.981 Gaps: 1

Percent Similarity: 97.101 Percent Identity: 95.652

alignment\_block:

US-09-016-869A-4 x T00745

Align seg 1/1 to: T00745 from: 1 to: 751

1 MetArgGluAsnLysGlyMetProSerGlyGlySerAspGlu1 17

|||||

335 ATGCGGAGGAGAACAAAGGCGATGCCAGTGGGGGGCGGCGATGAGG 384

17 yLeuAlaThr....ProAlaArgGlyLeuValGluLysValArgHisSerT 33

|||||

385 TC7GGCCAGCGCGCGCGGGGAGTAGTGGGAGAGGTCGACAGCTCC 434

33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49

|||||

435 TGAAGCGCGCGGATGCCAACGGAGTCAACCGTTTCGGAGGCGCGCG 484

50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeu 66

|||||

485 ATCCAGTCATGATGATGGCAGCGCGCGTGGCGAGCTGCTGCTGCT 534

66 uHisGlyAlaGluProAsnGlyValAsnArgPheGlyArgAla 83

|||||

535 CCACGGCGGGAGCCCACTGCGGACACCTGCGACTCTCACCCGACCGG 584  
 83 alHisAspAlaalaArgGluGlyPheLeuAspThrLeuValValLeuHis 99  
 |||||  
 585 TGCATGATGCTCCCGGAGGCTCTTGGACACGCTGGTGTGTGTCAC 634  
 100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProva 116  
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 635 CGGCGCGGGCGCGCTGACGTGCGGATGCTGGGTGCTGCTCCCGT 684  
 116 laspLeuAlaGluGlyArgGlyHisArgAspValAlaGlyTyrLeuArgT 133  
 |||||  
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 133 hrAlaThrGlyAsp 137  
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 735 CAGCCACGGGGGAC 748

seq\_name: N\_Geneseq\_36:Q99165

seq\_documentation\_block:

ID\_Q99165 standard; cDNA; 751 BP.

AC Q99165;

DT 03-MAR-1996 (first entry)

DE Human multiple tumour suppressor polypeptide, MTS2 encoding cDNA.

KW Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;

KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;

KW gene therapy; chronic; ds.

OS Homo sapiens.

FS Key Location/Qualifiers

FT cds 335..751

FT /\*tag= a

FT /product= MTS2

PN W09525429-A1.

PD 28-SEP-1995.

PE 17-MAR-1995; U03316.

PR 18-MAR-1994; US-214581.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215088.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 95-344401/44.

DR P-PSDB; R80948.

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences

PT - useful in diagnosis, prognosis and therapy of human cancer, e.g. .

PT melanoma or leukaemia

PS Claim 3; Page 102-103; 156pp; English.

CC The cDNA sequences encoding several multiple tumour suppressor (MTS)

CC polypeptides have been isolated and sequenced. This sequence encodes

CC the MTS polypeptide MTS2 (R80948). MTS polypeptide-encoding cDNAs

CC and mutants of these are useful for the diagnosis or prognosis of

CC human cancer. Germ-line mutations of MTS cDNAs can be used for

CC diagnosing predisposition to melanoma, leukaemia, astrocytoma,

CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers

CC of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and

CC rectum. The wild-type gene is useful for gene therapy and MTS

CC polypeptides may also be used for protein replacement therapy. Also

CC the polypeptides or cells contg. an altered MTS gene are useful for

CC screening for potential cancer therapeutics.

SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment\_scores:

Quality: 667.50

Ratio: 4.981

Percent Similarity: 97.101

Percent Identity: 95.652

Gaps: 1

Length: 138

alignment\_block:

US-09-016-869a-4 x Q99165

Align seg 1/1 to: Q99165 from: 1 to: 751

1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17  
 |||||  
 335 ATGCGGAGGAGAACAGGCGATGCCAGTGGGGCGGCACGATGAGGG 384  
 17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33  
 |||||  
 385 TCTGCCAGCCCGCGCGCGGAGCTAGTGAGAGAGGTGGACAGCTCC 434  
 33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49  
 |||||  
 435 TGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCG 484  
 50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66  
 |||||  
 485 ATCCAGTTCATGATGATGGGAGCGCGCGCTGGGAGAGCTGCTGCT 534  
 66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProv 83  
 |||||  
 535 CCACGGCGCGGAGCCCAACTGCGCAGACCCCTGCCACTCTCACCGACCGG 584  
 83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99  
 |||||  
 585 TGCATGATGCTCCCGGAGGCTCTTGGACACGCTGGTGTGTGTCAC 634  
 100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProva 116  
 |||||  
 635 CGGCGCGGGCGCGCTGACGTGCGGATGCTGGGTGCTGCTCCCGT 684  
 116 laspLeuAlaGluGlyArgGlyHisArgAspValAlaGlyTyrLeuArgT 133  
 |||||  
 685 GACRTTGGCCGAGGAGCGGGCCACCGCGACTTGCAGGGTACCTGCGCA 734  
 133 hrAlaThrGlyAsp 137  
 |||||  
 735 CAGCCACGGGGGAC 748  
 seq\_name: N\_Geneseq\_36:T69781  
 seq\_documentation\_block:  
 ID\_T69781 standard; cDNA; 751 BP.  
 AC T69781;  
 DT 10-SEP-1997 (first entry)  
 DE Human multiple tumour suppressor gene 2.  
 KW Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis; ds.  
 OS Homo sapiens.  
 FS Key Location/Qualifiers  
 FT cds 335..751  
 FT /\*tag= a  
 PN US5624819-A.  
 PD 29-APR-1997.  
 PE 18-MAR-1994; 214582.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03537.  
 PR 07-JUN-1995; US-474177.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI (UTAH ) UNIV UTAH RES FOUND.  
 PI Cannon-Albright LA, Kamb A, Skolnick MH;  
 DR WPI; 97-258217/23.  
 DR P-PSDB; W19255.  
 PT Human mutant multiple tumour suppressor gene sequences - for  
 PT production of recombinant mutant polypeptide(s)  
 PS Disclosure; Columns 75-78; 72pp; English.  
 CC The present sequence the human multiple tumour suppressor gene 2  
 CC (MTS2), useful in cancer diagnosis.  
 SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

```
alignment_scores:
  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
  Percent Similarity: 97.101  Percent Identity: 95.652

alignment_block:
  US-09-016-869A-4 x T69781 ..
  Align seg 1/1 to: T69781 from: 1 to: 751

1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
|||||
335 ATGCGCGAGGAGAACAGAGGCGATGCCAGTGGGGCGCGGATGAGGG 384
|||||
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
|||||
385 TCTGCCACAGCCCGCGCGGGGACTAGTGGAGAGGTGGCAGAGCTCC 434
|||||
33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
|||||
435 TGGAGCCGCGCGCGGATGCCAACGGAGTCAACCGTTTCGGAGGCGCG 484
|||||
50 lIeGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
|||||
485 ATCCAGGTGTCATGATGGCGAGCGCGCGCTGGCGAGCTGCTGCTGCT 534
|||||
66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
|||||
535 CCACGCGCGGAGCCCACTGCGCAGACCTGCCACTCTCACCCGACCGG 584
|||||
83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
|||||
585 TGCATGATGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTGTGTCAC 634
|||||
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
|||||
635 CGGCGCGGCGCGCGCTGGACGTGCGCGATGCCCTGGGGTCTGCTGCCGCT 684
|||||
116 lAspLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
|||||
685 GGACTTGGCCGAGGAGCGGGCCACCGCGACGTTTCAGGGTACCTGCGCA 734
|||||
133 hrAlaThrGlyAsp 137
|||||
735 CAGCCACGGGGGAC 748

seq_name: N_Geneseq_36:V11250

seq_documentation_block:
ID_V11250 standard; cDNA; 751 BP.
AC_V11250;
DT_15-JUL-1998 (first entry)
DE_Human MTS2 cDNA.
KW_MTS2: multiple tumour suppressor; diagnosis; cancer;
KW_germ-line mutation; familial melanoma locus; MLM; Predisposition; ds.
OS_Homo sapiens.
FH_Key Location/Qualifiers
FT_CDS 335..751
FT_/*tag= a
FT_/product= MTS2
FT_/note= "multiple tumour suppressor"
PN_US5739027-A.
PD_14-APR-1998.
PF_07-JUN-1995; 487033.
PR_07-JUN-1995; US-487033.
PR_18-MAR-1994; US-214582.
PR_18-MAR-1994; US-215086.
PR_18-MAR-1994; US-215087.
PR_14-APR-1994; US-227369.
PR_01-JUN-1994; US-251938.
PR_17-MAR-1995; WO-U03316.
PA (MYRI-) MYRIAD GENETICS INC.
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PI_Kamb A;
DR_WFI; 98-250421/22.
DR_P-PSDB; W40526.
PT_DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT_useful for the diagnosis of cancers related to MTS1E1-beta
PT_mutation(s) and their treatment
PS_Disclosure; Fig 11; 72pp; English.
CC_This cDNA sequence encodes a human multiple tumour suppression protein,
CC_MTS2. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
SQ_Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment_scores:
  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
  Percent Similarity: 97.101  Percent Identity: 95.652

alignment_block:
  US-09-016-869A-4 x V11250 ..
  Align seg 1/1 to: V11250 from: 1 to: 751

1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
|||||
335 ATGCGCGAGGAGAACAGAGGCGATGCCAGTGGGGCGCGGATGAGGG 384
|||||
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
|||||
385 TCTGCCACAGCCCGCGCGGGGACTAGTGGAGAGGTGGCAGAGCTCC 434
|||||
33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
|||||
435 TGGAGCCGCGCGCGGATGCCAACGGAGTCAACCGTTTCGGAGGCGCG 484
|||||
50 lIeGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
|||||
485 ATCCAGGTGTCATGATGGCGAGCGCGCGCTGGCGAGCTGCTGCTGCT 534
|||||
66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
|||||
535 CCACGCGCGGAGCCCACTGCGCAGACCTGCCACTCTCACCCGACCGG 584
|||||
83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
|||||
585 TGCATGATGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTGTGTCAC 634
|||||
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
|||||
635 CGGCGCGGCGCGCGCTGGACGTGCGCGATGCCCTGGGGTCTGCTGCCGCT 684
|||||
116 lAspLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
|||||
685 GGACTTGGCCGAGGAGCGGGCCACCGCGACGTTTCAGGGTACCTGCGCA 734
|||||
133 hrAlaThrGlyAsp 137
|||||
735 CAGCCACGGGGGAC 748

seq_name: N_Geneseq_36:V53831

seq_documentation_block:
ID_V53831 standard; cDNA; 751 BP.
AC_V53831;
DT_04-DEC-1998 (first entry)
DE_Coding sequence 2 of the multiple tumour suppressor MTS1E1S.
DE_Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
KW_somatic mutation; gene therapy; ds.
OS_Homo sapiens.
```

```

FH Key          Location/Qualifiers
FT CDS          335..751
FT FT           /*tag= a
FT product= "human MTS1E1s"

US5801236-A.
PD 01-SEP-1998.
PD 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 98-494842/42.
DR P-PSDB; W74553.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Disclosure; Fig 11: 73pp; English.
CC This is the nucleotide sequence of the multiple tumour suppressor
CC (MTS1E1s) gene, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment_scores:
Quality: 667.50 Length: 138
Ratio: 4.981 Gaps: 1
Percent Similarity: 97.101 Percent Identity: 95.652

alignment_block:
US-09-016-869A-4 x V53831 ..
Align seg 1/1 to: V53831 from: 1 to: 751

1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
|||||
335 ATGCGCGAGGAGAACAAAGGGCATGCCAGTGGGGCGGCGAGCGATGAGG 384
|||||
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
|||||
385 TCTGGCAGCCCGCGCGGGGACATAGTGGAGAAAGGTGCGAGCTCC 434
|||||
33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
|||||
435 TGGAAAGCGGGCGGATCCCAACAGAGTCAACCGTTTCGGAGGCGGCG 484
|||||
50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
|||||
485 ATCCAGGTCTATGATGATGGGCGAGCGCGCGTGGCGAGCTGCTGCT 534
|||||
66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 83
|||||
535 CCACGGCGGGAGCCCAACTCGCGAGACCTTCGCCCTCTACCCGACCGG 584
|||||
83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
|||||
585 TGCATGATGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGTCTGCAC 634
|||||
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116

```

```

|||||
635 CGGGCGGGCGCGCTGACGTGCGATGCTGGGTGCTGCTGCCCT 684
|||||
116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
|||||
685 GGACTTGGCGGAGGAGCGGGCCACCGCCAGCTTGCGAGGTACCTGCGCA 734
|||||
133 hrAlaThrGlyAsp 137
|||||
735 CAGCCACGGGGGAC 748

seq_name: N_Geneseq_36:V70595

seq_documentation_block:
ID V70595 standard; cDNA; 751 BP.
AC V70595;
DT 03-FEB-1999 (first entry)
DE cDNA encoding a human multiple tumour suppressor 2 (MTS2) protein.
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Homo sapiens.
FH Key          Location/Qualifiers
FT CDS          335..751
FT FT           /*tag= a
FT misc_feature 490..491
FT FT           /*tag= b
FT FT           /*note= "splice site"
FT US5843756-A.
PD 01-DEC-1998.
PR 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI: 99-044585/04.
DR P-PSDB; W80526.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 6; Fig 11; 80pp; English.
CC The present sequence encodes a human multiple tumour suppressor 2
CC (MTS2) protein. The sequence is homologous to the corresponding
CC murine gene. Primers designed from the gene can be used to design
CC primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment_scores:
Quality: 667.50 Length: 138
Ratio: 4.981 Gaps: 1
Percent Similarity: 97.101 Percent Identity: 95.652

alignment_block:
US-09-016-869A-4 x V70595 ..
Align seg 1/1 to: V70595 from: 1 to: 751

1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
|||||
335 ATGCGCGAGGAGAACAAAGGGCATGCCAGTGGGGCGGCGAGCGATGAGG 384
|||||
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
|||||
385 TCTGGCAGCCCGCGCGGGGACATAGTGGAGAAAGGTGCGAGCTCC 434
|||||
33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
|||||
435 TGGAAAGCGGGCGGATCCCAACAGAGTCAACCGTTTCGGAGGCGGCG 484
|||||
50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
|||||
485 ATCCAGGTCTATGATGATGGGCGAGCGCGCGTGGCGAGCTGCTGCT 534
|||||

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alignment_scores:
  Quality: 554.00      Length: 134
  Ratio: 4.541        Gaps: 2
  Percent Similarity: 91.045  Percent Identity: 84.328

alignment_block:
  US-09-016-869A-4 x T02964

  Align seg 1/1 to: T02964 from: 1 to: 580

      5 AsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLeuAlaThr... 20
      82 GACAGGGGATG...TTGGGCGGCGAGCTGACGCGGGCTGGCCACCGC 128
      21 ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
      129 CGCGCGCGGGGCAAGTGGAGACAGCGTGGCGGAGCTCTGGGAAGCGGCG 178
      37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
      179 CAGATCCCAACCCCTGACACCGCTTCGGGAGCGGCCCAATCCAGGTCATG 228
      54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyValAc 70
      229 ATGATGGGCGAGCGCCAGGTGGCAGAGCTGCTGCTCCAGGAGCAGA 278
      70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
      279 ACCCAACTCGCGCGACCCCTGCCACCTTACCAGACCTGTGACGACGCGAG 328
      87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
      329 CTCGGGAGGCTTCTGGACACGCTTGTGCTGCACCGGGCGGCGGCG 378
      104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaCl 120
      379 CGGTTGGATGTGTGACCGCTGGGCGGCGCTGCGCGGTAGACTTGGCTGA 428
      120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGlyA 137
      429 AGAGCAGGGGCCACCGTGACATGCGAGGTATCTGCACGCTGCCACTGGAG 478
      137 sp 137
      479 AT 480

seq_name: N_Geneseq_36:V70624

seq_documentation_block:
  ID V70624 standard; cDNA; 393 BP.
  DT 03-FEB-1999 (first entry)
  DE Mouse multiple tumour suppressor 2 gene (MTS2) coding sequence.
  KW Murine; multiple tumour suppressor 2 gene; MTS2; cancer; ss.
  OS Mus musculus.
  FH Key Location/Qualifiers
  FT CDS 1..393 /*tag= a
  FT misc_feature 132..133 /*tag= b
  FT /*note= "splice site"
  FT US5843756-A.
  PN 01-DEC-1998.
  PD 28-JUL-1995; 058735.
  PR 28-JUL-1995; US-508735.
  PR 07-JUN-1995; US-487033.
  PA (MIRI-) MIRIAD GENETICS INC.
  PI Jiang P, Kamb A, Stone S;
  DR WPI; 99-044585/04.
  DR P-PSDB; W70823.
  PT Mouse multiple tumour suppressor gene segment - useful for primer design

```

```

PS Example 7; Fig 18; 80pp; English.
CC The present sequence encodes mouse multiple tumour suppressor 2
CC (MTS2) gene. The MTS1 gene can be used to design primers to
CC detect abnormalities i.e. polymorphisms which may predispose
CC towards malignancies such as melanoma, leukaemia, astrocytoma,
CC lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 393 BP; 69 A; 124 C; 141 G; 59 T;

alignment_scores:
  Quality: 545.50      Length: 128
  Ratio: 4.623        Gaps: 1
  Percent Similarity: 92.188  Percent Identity: 85.156

alignment_block:
  US-09-016-869A-4 x V70624

  Align seg 1/1 to: V70624 from: 1 to: 393

      11 GlyGlyGlySerAspGluGlyLeuAlaThr...ProAlaArgGlyLeuVa 26
      7 GCGGCGACGACGTGACGCGGGCTGCGCCACCGCGCGCGGGGCAAGT 56
      26 lGluLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyVala 43
      57 GGAGACGGTGGCGCAACTCTCTGGAAGCGGCGGACAGATCCCAACGCCCTGA 106
      43 snArgPheGlyArgAlaIleGlnValMetMetMetGlySerAlaArg 59
      107 ACCGCTCGGGAGGCGCCCAATCCAGGTATGATGATGGCGGCGCCAG 156
      60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76
      157 GTGCGAGAGCTGCTGCTCCACGAGGAGACCCCAACTGCGCGGACCC 206
      76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA 93
      207 TGCACCCCTTACCAGACCTGTGCACGACGCGGAGCTCGGGAGGCTTCCTGG 256
      93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
      257 ACAGCTTGTGCTGCTGCACCGGCGGCGGCGGCTGGATGTGTGTGAC 306
      110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126
      307 GCCTGGGCGGCGCTGCGGTAGACTTGGCTGAAGAGCAGGCGGCCACCGTGA 356
      126 pValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
      357 CATTCGAGGTATCTGCACGCTGCCACTGGAGAT 390

seq_name: N_Geneseq_36:X26232

seq_documentation_block:
  ID X26232 standard; DNA; 1073 BP.
  AC X26232;
  DT 25-MAY-1999 (first entry)
  DE Truncated p27/p16 fusion protein encoding DNA.
  KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
  KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
  KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
  KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
  KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
  KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
  KW tachycardia; human; p27; p16; truncated; ss.
  OS Homo sapiens.
  PN W0906540-A2.
  PD 11-FEB-1999.
  PR 29-JUL-1998; U15759.
  PR 29-JUL-1997; US-902572.
  PA (MITO-) MITOTIX INC.
  PI Beach DH, Gyuris J, Lamphere L;

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```
DR WPI; 99-153770/13.
PT Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60; Page 83-84; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p27/p16 fusion
CC protein.
SQ Sequence 1073 BP; 215 A; 317 C; 388 G; 153 T;

alignment_scores:
  Quality: 513.00      Length: 158
  Ratio: 4.347        Gaps: 2
  Percent Similarity: 74.684      Percent Identity: 70.253

alignment_block:
US-09-016-869A-4 x X26232 ..
Align seg 1/1 to: X26232 from: 1 to: 1073

3 GluGluAsnLysGlyMetProSerGlyGlySerAspGluGly..... 17
||||| : : : : : : : : : : : : : : : : : : : :
526 GAAGAAAATGTTTCAGACGGTGTGGCGGGGCGACGGGGTGGCGGTC 575
17 .....

576 CGCGCGGGGTGGATCCGTCGAGGATCCGGCGGGGAGCAGCATGGAGC 625
18 .....LeuAlaThr...ProAlaArgGlyLeuValGluLys 28
||||| : : : : : : : : : : : : : : : : : : : :
626 CTTCCGGCTGACTGGTGCACCGCGCGCGCGGGTGGGTAGAGGAG 675
29 ValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyValAsnArgPh 45
||||| : : : : : : : : : : : : : : : : : : : :
676 GTGCGGCGCTGCTGGAGCGGGGGCGCTGCCCAACGCCAATAGTTA 725
45 eGlyArgArgAlaIleGlnValMetMetMetGlySerAlaArgValAlaG 62
:||||| : : : : : : : : : : : : : : : : : : : :
726 CGGTGCGAGCGCGATCCAGGTCAATGATGCGGAGCGCCCGAGTGCGG 775
62 luLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThr 78
||||| : : : : : : : : : : : : : : : : : : : :
776 AGCTGCTGCTCTCCACGGCGCGAGCCCAACTGCGCGGACCCCGCACT 825
79 LeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThrLe 95
||||| : : : : : : : : : : : : : : : : : : : :
826 CTCACCGACCGGTGCACAGCGCTGCCCGGAGGGGCTTCCTGGACAGCT 875
95 uValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpG 112
||||| : : : : : : : : : : : : : : : : : : : :
876 GGTGGTGTGACCGCGGGCGGGCGGGCTGGAGCTGCGCGCATGCTGGG 925
112 lyArgLeuProValAspLeuAlaGluAlaArgGlyHisArgAspValAla 128
||||| : : : : : : : : : : : : : : : : : : : :
926 GCCGTCTGCCCGTGGAGCTGGCTGAGGAGCTGGGCCATCGCGATGTCGA 975
129 GlyTyrLeuArgThrAlaThrGly 136
```

```
||||| : : : : : : : : : : : : : : : : : : : :
976 CGGTACTCGCGCGCGCTGCGGG 999

seq_name: N_Geneseq_36:X26234
seq_documentation_block:
ID X26234 standard; DNA; 782 BP.
AC X26234;
DT 25-MAY-1999 (first entry)
DE Truncated p27/p16 fusion protein encoding DNA.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated; ss.
OS Homo sapiens.
PN WO906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI; 99-153770/13.
DR P-PSDB; W95106.
PT Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60; Page 85; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p27/p16 fusion
CC protein.
SQ Sequence 782 BP; 137 A; 236 C; 295 G; 114 T;

alignment_scores:
  Quality: 509.00      Length: 144
  Ratio: 4.426        Gaps: 2
  Percent Similarity: 79.861      Percent Identity: 75.694

alignment_block:
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7 GlyMetProSerGlyGlySerAspGluGly..... 17
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277 GCGGTTCCGCGGGGTGGATCCGTCGAGGATCCGCGGGGGGAGCAG 326
18 .....LeuAlaThr...ProAlaArgGlyLeuV 26
||||| : : : : : : : : : : : : : : : : : : : :
327 CATGAGACCTTCGCTGACTGGCTGCGCACGCGCGCGGGTTCGGG 376
26 alGluLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyVal 42
||||| : : : : : : : : : : : : : : : : : : : :
377 TAGAGAGAGGTGCGGGCGCTGCTGAGGCGGGGGCGCTGCCCAACGACCG 426
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CC mutated sequences are those that are present in somatic mutations  
 CC of the gene in cancers. The vectors can be used for gene therapy  
 CC strategies to replace function of mutated protein in patients. These  
 CC can also be used to construct protein mimetics, also for therapeutic  
 CC strategies. In addition the expression constructs can also be used  
 CC for recombinant production of MTS. Recombinant MTS can be used to  
 CC screen for drugs to be used for cancer therapy, and the protein  
 CC itself may also be used to restore MTS function in a cell.  
 SQ Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;

alignment\_scores:  
 Quality: 506.50 Length: 133  
 Ratio: 4.404 Gaps: 2  
 Percent Similarity: 86.466 Percent Identity: 80.451  
 alignment\_block:  
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 Align seg 1/1 to: V53819 from: 1 to: 471

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9 ProSerGlyGlySerAspGlu.....GlyLeuAlaThr.. 20
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57 CGCGCGCGGGGTCGGTAGAGGAGTTCGGGCGCTGCTGCCAGCGGGG 106

37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
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107 CGTGCCACAGCCACCAATAGTTACGGTCGGAGCGCATCCAGTCTATG 156

54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
||||| |||:||||:||||| |||
157 ATGATGGCAGCGCCGAGTGGCGAGTGTCTGTCTCCACGCGCGGA 206

70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAla 87
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207 GCCCACTGGCGGACCCGCCACTCTCACCCGACCGCTGCACACGCTG 256

87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
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257 CCGCGGAGGCTTCCTGGACAGCTGTGTGTGTGCTGCACCGCGCGGGCG 306

104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
||||| |||:||||:||||| |||
307 CGGTGGACGTGCGCATGCTTGGGCGCTGTGCCCGTGGACCTGGCTGA 356

120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
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357 GGAAGCTGGGCATCGCATGTCGCACGATACCTCGCGCGGCTCGGGG 405

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seq\_name: N\_Geneseq\_36:V70583

seq\_documentation\_block:  
 ID V70583 standard; cDNA; 471 BP.  
 AC V70583;  
 DT 03-FEB-1999 (first entry)  
 DE cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.  
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..471  
 FT misc\_feature 150..151  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /\*note= "splice site"  
 FT 478..458  
 FT /\*tag= c  
 FT /\*note= "splice site"  
 PN US5843756-A.  
 PD 01-DEC-1998.

PF 28-JUL-1995; 058735.  
 PR 28-JUL-1995; US-508735.  
 PR 07-JUN-1995; US-487033.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI Jiang P, Kamb A, Stone S;  
 DR WPI: 99-044585/04.  
 DR P-PSDB; W80524.  
 PT Mouse multiple tumour suppressor gene segment - useful for primer design  
 PS Disclosure: Columns 63-66; 80pp; English.  
 CC The present sequence encodes a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.  
 SQ Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;

alignment\_scores:  
 Quality: 506.50 Length: 133  
 Ratio: 4.404 Gaps: 2  
 Percent Similarity: 86.466 Percent Identity: 80.451  
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57 CGCGCGCGGGGTCGGTAGAGGAGTTCGGGCGCTGCTGCCAGCGGGG 106

37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
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107 CGTGCCACAGCCACCAATAGTTACGGTCGGAGCGCATCCAGTCTATG 156

54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
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157 ATGATGGCAGCGCCGAGTGGCGAGTGTCTGTCTCCACGCGCGGA 206

70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAla 87
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207 GCCCACTGGCGGACCCGCCACTCTCACCCGACCGCTGCACACGCTG 256

87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
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257 CCGCGGAGGCTTCCTGGACAGCTGTGTGTGTGCTGCACCGCGCGGGCG 306

104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
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307 CGGTGGACGTGCGCATGCTTGGGCGCTGTGCCCGTGGACCTGGCTGA 356

120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
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357 GGAAGCTGGGCATCGCATGTCGCACGATACCTCGCGCGGCTCGGGG 405

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seq\_name: N\_Geneseq\_36:X26233

seq\_documentation\_block:  
 ID X26233 standard; DNA; 737 BP.  
 AC X26233;  
 DT 25-MAY-1999 (first entry)  
 DE Truncated p27/p16 fusion protein encoding DNA.  
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;





428 AGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGCGCGGATC 477  
51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 67  
|||||  
478 CAGGTATGATGATGGCAGCGCGCGGTGGCGAGTGTCTGCTCCA 527  
67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84  
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528 CGCGCGGAGGCCAACTCGCAGACCGCTGCACCTCACCCGCGGTGC 577  
84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100  
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578 ATGATGCTGCCGGAGGCTTCTGACACGCTGGTGGTGGTGCACCG 627  
101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 117  
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628 GCCGGCGCGCGGTGGACGTGCGCATGCTGGGTGCTGCTGCCGTGGA 677  
117 pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThra 134  
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678 CTGGCGGAGGAGCGGGGCCACCGGACGTTGCAGGGTACCTCGGCACAG 727  
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seq\_name: /cgn2\_6/ptodata/1/ina/5D\_COMB.seq:US-08-893-274-3

seq\_documentation\_block:  
; Sequence 3, Application US/08893274  
; Patent No. 5968821  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,  
; TITLE OF INVENTION: and Uses Related Thereto  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,274  
; FILING DATE: 15-JULY-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEPTEMBER-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APRIL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOVEMBER-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DECEMBER-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/963,308  
; FILING DATE: 16-OCTOBER-1992

ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-071.09  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 837 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 328..738  
US-08-893-274-3

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Quality: 717.00 Length: 137  
Ratio: 5.234 Gaps: 0  
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alignment\_block:

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17 yLeuAlaThrProAlaArgGlyLeuValGluLysValArgHisSerTrpG 34  
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378 TGTGCCACCGCGCGCGGGGACTAGTGGAGAGGTGGCACACTCTCTGGG 427  
34 luAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAlaIle 50  
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428 AAGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGCGCGGATC 477  
51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 67  
|||||  
478 CAGGTATGATGATGGCAGCGCGCGCTGGCGAGCTGCTGCTCCA 527  
67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84  
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528 CGCGCGGAGCGCGCGCGCGAGACCTGCGCAGACCTCTCACCCGCGGTGC 577  
84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100  
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578 ATGATGCTGCCGGAGGCGCTTCTTGGACACGCTGGTGGTGGTGCACCG 627  
101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 117  
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628 GCCGGCGCGCGCTGGACGTGCGCATGCTGGGTGCTGCTGCCGTGGA 677  
117 pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThra 134  
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728 CCACGGGGGAC 738

seq\_name: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:US-08-474-177-15

seq\_documentation\_block:  
; Sequence 15, Application US/08474177  
; Patent No. 5624819  
; GENERAL INFORMATION:  
; APPLICANT: Skolnick, Mark H.



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; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GENE LINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; US-08-474-177-15

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  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
Percent Similarity: 97.101 Percent Identity: 95.652

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33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
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66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
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635 CGGGCGGGCGCGCGCTGGACGTGCGCGATGCTGGGGTCTGCTGCCGT 684
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; Sequence 15, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
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; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
; US-08-487-033-15

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    Quality: 667.50      Length: 138
    Ratio: 4.981        Gaps: 1
    Percent Similarity: 97.101  Percent Identity: 95.652

alignment_block:
US-09-016-869a-4 x US-08-487-033-15

Align seg 1/1 to: US-08-487-033-15 from: 1 to: 751

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; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
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; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
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; FILING DATE: 18-MAR-1994
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; FILING DATE: 18-MAR-1994
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; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
; US-08-480-810-15

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alignment_scores:
    Quality: 667.50      Length: 138
    Ratio: 4.981        Gaps: 1
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17 yLeuAlaThr...ProAlaArgGlyLeuValLysValArgHisSerT 33
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385 TCTGCCAGCGCCGCGCGGAGCTAGTGGAGAGGTGCACAGCTCC 434

33 rpGluAlaGlyAlaAspProAsnGlyValAlaGluLeuLeuLe 66
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435 TGGAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGCG 484

50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
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485 ATCCAGGTCATGATGATGGCAGCGCCCGCGTGGGGAGCTGCTGCT 534

66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
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535 CCACGGCGCGGAGCCCAACTGCCAGACCTGCCACTCTCACCGACGG 584

83 alHisAspAlaAlaArgGlyPheLeuAspThrLeuValValLeuHis 99
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585 TGCATGATGCTGCCCGGAGGCTTCTTGGACAGCGCTGCTGCTGCAC 634

100 ArgAlaGlyAlaArgLeuAspValArgAspAlaThrPglyArgLeuProVa 116
|||||
635 CGGGCCGGGGCGCGCTGGAGCTGGCGATGCCCTGGGGTCTGCTGCCCGT 684

116 lAspLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
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685 GGACTTGGCGGAGGCGGGGCCACCGGACGTTGCAGGTTACCTGCACA 734

133 hrAlaThrGlyAsp 137
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735 CAGCCACGGGGGAC 748

seq_name: /cgn2_6/ptodata/1/lna/5C_comb.seq:US-08-508-735-15

seq_documentation_block:
; Sequence 15, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
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735 CAGCCACGGGGGAC 748

seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-848-251-15

seq_documentation_block:
; Sequence 15, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,251
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/474,083
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751

US-08-848-251-15

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Percent Similarity: 97.101 Percent Identity: 95.652

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|||||
385 TCTGCCACGCGCGCGCGGACTAGTGGAGAAAGGTGGCAGACTCC 434
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33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
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66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
|||||
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83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
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seq_documentation_block:
; Sequence 15, Application US/08486047
; Patent No. 5994095
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
; US-08-486-047-15

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    Quality: 667.50      Length: 138
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    Percent Similarity: 97.101      Percent Identity: 95.652

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Align seg 1/1 to: US-08-486-047-15 from: 1 to: 751

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17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisserT 33
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385 TCTGCCAGCGCCCGCGCGCGGAGCTAGTGAGAGAGTGCGCAGCTCC 434
|||||
33 rpGluAlaGlyAlaAspProAsnGlyValAsnA-gPheGlyArgAla 49
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435 TGGAGCGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGC 484
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116 lAspLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
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735 CAGCCACGGGGGAC 748

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seq_documentation_block:
; Sequence 15, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: 08/480,810
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
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;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
US-09-120-130-15

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  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
  Percent Similarity: 97.101  Percent Identity: 95.652

alignment_block:
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535 CCACGCGCGGAGCGCAACTGCGCAGACCTGCCACTCCACCCGACCGG 584
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585 TGCATGATGCTGCCGGGAGGGCTTCTGGACACGCTGGTGGTGCAC 634
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100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
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116 lAspLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
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133 hrAlaThrGlyAsp 137
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735 CAGCCACGGGGAC 748

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seq_documentation_block:
; Sequence 15, Application US/09115252
; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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83 aHIsaspaLaalargLuGluGlypHeLeuaspThrLeuValValLeuHis 99  
588 TGCATGATGCTCCCGGAGGGGCTTCGTGGACAGCGTGGTGGCTGCAC 637  
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116 lAspLeuAlaGluGluArGyGlyHisArgAspValAlaGlyTyrLeuArg 133  
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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and U
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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; PCT-US95-04636-3

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  Percent Similarity: 97.101  Percent Identity: 95.652

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, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/497,214
, FILING DATE: 30-JUN-1995
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/346,147
, FILING DATE: 29-NOV-1994
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, FILING DATE: 25-MAY-1994
, PRIOR APPLICATION DATA:
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, FILING DATE: 14-APR-1994
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/154,915
, FILING DATE: 18-NOV-1993
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/991,997
, FILING DATE: 17-DEC-1992
, ATTORNEY/AGENT INFORMATION:
, NAME: Vincent, Matthew P.
, REGISTRATION NUMBER: 36,709
, REFERENCE/DOCKET NUMBER: MIV-071.06
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (617) 832-1299
, TELEFAX: (617) 832-7000
, INFORMATION FOR SEQ ID NO: 3:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 850 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: both
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
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, NAME/KEY: CDS
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US-08-581-918A-3

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  Ratio: 4.981      Gaps: 1
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MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WordPad
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    FILING DATE: 30-JUN-1995
  APPLICATION DATA:
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    FILING DATE: 29-NOV-1994
  APPLICATION DATA:
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    FILING DATE: 14-SEP-1994
  APPLICATION DATA:
    APPLICATION NUMBER: US 08/248,812
    FILING DATE: 25-MAY-1994
  APPLICATION DATA:
    APPLICATION NUMBER: US 08/227,371
    FILING DATE: 14-APR-1994
  APPLICATION DATA:
    APPLICATION NUMBER: US 08/154,915
    FILING DATE: 18-NOV-1993
  APPLICATION DATA:
    APPLICATION NUMBER: US 07/991,997
    FILING DATE: 17-DEC-1992
  ATTORNEY/AGENT INFORMATION:
    NAME: Vincent, Matthew P.
    REGISTRATION NUMBER: 36,709
    REFERENCE/DOCKET NUMBER: MIV-071.06
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617) 832-1299
      TELEFAX: (617) 832-7000
    INFORMATION FOR SEQ ID NO: 7:
      SEQUENCE CHARACTERISTICS:
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        TYPE: nucleic acid
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        TOPOLOGY: linear
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US-09-016-869a-4

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21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
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gb_est37:AI916967	+	226.00	426.52	6.3e-15	522	!	AI916967	ts7d01.x1	NCI_CGAP
gb_est36:AI869175	-	226.00	425.81	6.3e-15	563	!	AI869175	w150c04.x1	NCI_CGAP
gb_est18:AI280099	+	225.00	423.98	8.7e-15	558	!	AI280099	qk47d01.x1	NCI_CGAP
gb_est45:AI762172	+	223.00	421.63	1.2e-14	475	!	AI762172	wh90g02.x1	NCI_CGAP

seq\_documentation\_block:

LOCUS	AI394605	566 bp	mRNA	EST	30-MAR-1999
DEFINITION	tgi3905.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108696 3', similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A ; contains LTR9.b3 TAR1 repetitive element ; , mRNA sequence.				
ACCESSION	AI394605				
VERSION	AI394605.1	GI:4224152			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo				

ALPHA  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

(Accessed 11/03/07)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov

CDNA Library Preparation: M. Danto Sources/ Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.

```

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert length: 755 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 457.

FEATURES
    source
        1..566
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2108696"
            /clone_lib="NCI_CGAP_CLL1"
            /tissue_type="B-cell, chronic lymphocytic leukemia"
            /lab_host="DH10B"
            /note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTCAAGTGGGCGGCGCATGCTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      113 a      159 c      175 g      118 t      1 others
ORIGIN

alignment_scores:
    Quality: 430.00      Length: 92
    Ratio: 4.943      Gaps: 0
    Percent Similarity: 94.565      Percent Identity: 91.304

alignment_block:
    US-09-016-869A-4 x AI394605/rev ..

Align seg 1/1 to reverse of: AI394605 from: 1 to: 566

45  PheGlyArgArgAlaIleGlnValMetMetMetGlySerAlaArgValAl 61
    ::::::::::|::::::::::::::::::::::::::|
566  TACGTCGGAGGCCGCATCAGGTCTGATGATGGCGCGCGCGAGTGCC 517

```

61 agluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaT 78  
 516 GGAGCTGCTGCTCCACGGCGGAGCCCACTGCGCNGACCCGCCA 467  
 78 hrLeuThrArgProValHisAspAlaAaArgGluGlyPheLeuAspThr 94  
 466 CTCTCACCGACCGGTGCACGAGTCCCGGGAGGCTTCTTCGACAGC 417  
 95 LeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTr 111  
 416 CTGTGGTCTGCTACCGCGCGGCGCGCTGGACGTGCGGATGCTG 367  
 111 pGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAspValA 128  
 366 GGGCGCTGCTGCGCGGAGCTGGCTGAGGAGTGGGCCATCGGATGCTG 317  
 128 laGlyTyrLeuArgThrAlaThrGly 136  
 316 CACGGTACTGCGCGGCTGCGGGG 291

seq\_name: gb\_est41:AW328496

seq\_documentation\_block: 648 bp mRNA EST 28-JAN-2000  
 LOCUS AW328496 ds02h12.x1 NIH\_MGC\_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA  
 DEFINITION sequence.

ACCESSION AW328496

VERSION AW328496.1 GI:6798992

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS 1 (bases 1 to 648)

TITLE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

On Apr 7, 1998 this sequence version replaced gi:3036295.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Edge Biosystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Plate: LLCM0030 row: 0 column: 24

Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers

1. 648

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2847599"

/clone\_lib="NIH\_MGC\_4"

/cell\_line="MGCL"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: Cervix; Vector: pOTB7a; Site\_1: Scel;

Site\_2: Ceul; cDNA made by oligo-dT priming.

Directionally cloned into Ceul/Scel sites using the

following 5' adaptor: taactatacgtcttaaggtagcga and 3'

adaptor: ttctaccctcttcgccaccacataaa. Average

insert size 900 bp. Library prepared by Edge Biosystems.

BASE COUNT 127 a 200 c 196 g 123 t 2 others

ORIGIN

alignment\_scores:

Quality: 423.00 Length: 101

Ratio: 4.648 Gaps: 1

Percent Similarity: 90.099 Percent Identity: 86.139

alignment\_block:

US-09-016-869A-4 x AW328496 ..

Align seg 1/1 to: AW328496 from: 1 to: 648

36 GlyAlaAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnVa 52  
 70 GGAGCCAGCGTCTAGGCGCAGCAGCGCTTC.....CTAGAAGACCAAGT 113  
 52 lMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyA 69  
 114 CATGATGATGGCAGCGCCCGAGTGGGAGACTGCTGCTGTCTCCACGGCG 163  
 69 laGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisasp 85  
 164 CGGAGCCCAACTGCGCGCAGCCCGCCACTCTCACCCGACCGTGCACGAC 213  
 86 AlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGl 102  
 214 GCTGCCCGGGAGGCTTCCTGGACACGCTGGTGTGTGCACCGGCGCGG 263  
 102 YAlaArgLeuAspValArgAspAlaTipGlyArgLeuProValAspLeuA 119  
 264 GCGCGGCTGACGCTGCGGATGCTGGGCGGCTGCTGCCGTGGACCTGG 313  
 119 laGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThr 135  
 314 CTGAGGAGCTGGCGCATCGCGATGTCGACGCTACCTGCGGCGGCTGCG 363  
 136 Gly 136  
 364 GGG 366

seq\_name: gb\_est26:AI871381

seq\_documentation\_block:

LOCUS AI871381 590 bp mRNA EST 07-MAR-2000  
 DEFINITION w181d11.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3'  
 similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
 ; mRNA sequence.

ACCESSION AI871381

VERSION AI871381.1 GI:5545430

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 590)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

On Oct 30, 1998 this sequence version replaced gi:3813427.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 845 Std Error: 0.00

Seq primer: -400P from G1bco

High quality sequence stop: 444.

Location/Qualifiers

1. .590

/organism="Homo sapiens"

FEATURES

source

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/db_xref="taxon:9606"
/clone="IMAGE:2431317"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCCGATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      114 a   158 c   179 g   139 t
ORIGIN

alignment_scores:
  Quality: 420.00      Length: 86
  Ratio: 5.000        Gaps: 0
  Percent Similarity: 97.674  Percent Identity: 95.349

alignment_block:
US-09-016-869A-4 x AI871381/rev ..

Align seg 1/1 to reverse of: AI871381 from: 1 to: 590

51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi 67
|||||
566 CAGGTCATGATGATGGGAGCGGAGGAGTGGCGGAGCTGCTGCTGCCA 517
|||||

67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||

516 CGGCGGGAGCGCAACTCGCGGACCGCCGCACTCTCACCAGCCCGTGC 467
|||||

84 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||

466 ACGACGCTGCCCGGAGGCGCTCTCGGACAGCTGGTGGTGTGCACCGG 417
|||||

101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
|||||

416 GCCGGGGCGCGCTGGAGCTGGCGGATGCTGGGCGCTGCTGCCGTGA 367
|||||

117 pLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
|||||

366 CTGGCTGAGGAGCTGGGCCATCGCATGCGCAGCTACCTGCGCGGG 317
|||||

134 laThrGly 136
|||||
316 CTGCGGGG 309

seq_name: gb_est36:AI870879

seq_documentation_block:
LOCUS      AI870879      579 bp      mRNA      EST      07-MAR-2000
DEFINITION w177d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430933 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION  AI870879
VERSION    AI870879.1 GI:5544847
KEYWORDS  EST.
SOURCE     human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute / National Institute of Neurological
TITLE     Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL   Unpublished (1998)
COMMENT   On May 18, 1998 this sequence version replaced gi:3136959.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 819 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 474.
FEATURES
  Location/Qualifiers
    1..579
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:2430933"
      /clone_lib="NCI_CGAP_Brn25"
      /tissue_type="anaplastic oligodendroglioma"
      /lab_host="DH10B"
      /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCCGATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
    BASE COUNT      113 a   157 c   182 g   127 t
    ORIGIN

alignment_scores:
  Quality: 408.00      Length: 86
  Ratio: 4.976        Gaps: 0
  Percent Similarity: 95.349  Percent Identity: 93.023

alignment_block:
US-09-016-869A-4 x AI870879/rev ..

Align seg 1/1 to reverse of: AI870879 from: 1 to: 579

51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 67
|||||
555 CAGGTCATGATGATGGGAGCGGAGGAGTGGCGGAGCTGCTGCTGCCA 506
|||||

67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||

505 CGGCGGGAGCGCAACTCGCGGACCGCCGCACTCTCACCAGCCCGTGC 456
|||||

84 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||

455 ACGACGCTGCCCGGAGGCGCTCTCGGACAGCTGGTGGTGTGCACCGG 406
|||||

101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
|||||

405 GCCGGGGCGCGCTGGAGCTGGCGGATGCTGGGCGCTGCTGCCGTGA 356
|||||

117 pLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
|||||

355 CTGGCTGAGGAGCTGGGCCATCGCATGCGCAGCTACCTGCGCGGG 306
|||||

134 laThrGly 136
|||||
305 CTGCGGGG 298

seq_name: gb_est17:AI198233
seq_documentation_block:
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Percent Similarity: 95.349 Percent Identity: 91.860

# alignment\_block:

US-09-016-869A-4 x AI362049/rev ..

Align seg 1/1 to reverse of: AI362049 from: 1 to: 580

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51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuH 67
|||||
556 CAGGTGATGATGGCAGCGCTCGAGTGGCGGAGCTGCTGCTCCA 507
|||||
67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||
506 CGCGCGGAGCCCACTGCGCGGAGCTCCGCCACTCACCACCGACCTGC 457
|||||
84 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||
456 ACGAGCTGCCCGGAGGCTTCTGAACACAGCTGTGTGTGCACCGG 407
|||||
101 AlaGlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValAs 117
|||||
406 GCGCGGCGCGGCTGACGTGCGGATGCTGCGGCGCTGCTGCCGTGA 357
|||||
117 pLeuAlaGluAlaArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
|||||
356 CTGGCTGAGGAGCTGGGCGCATCGCATGTCGCACGGTACCTACCTGCGGCGG 307
|||||
134 laThrGly 136
|||||
306 CTGCGGGG 299

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seq\_name: gb\_est25:AI765096

# seq\_documentation\_block:

LOCUS AI765096 774 bp mRNA EST 21-DEC-1999  
DEFINITION w448b08.x1 NCI-CGAP Col6 Homo sapiens cDNA clone IMAGE:2393463 3' similar to TR:Q13399 Q13399 HYPONHEICAL 18.1 KDA PROTEIN ; contains LTR9.b3 MER22 repetitive element ; , mRNA sequence.

ACCESSION AI765096  
VERSION AI765096.1 GI:5231605  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 774)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
On Feb 22, 1999 this sequence version replaced gi:4283180.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/Image.html](http://www-bio.llnl.gov/bbrp/image/Image.html)  
Insert Length: 854 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 400.  
Location/Qualifiers  
1..774  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2393463"  
/clone\_lib="NCI-CGAP Col6"  
/tissue\_type="colon tumor, RER+"  
/lab\_host="DH10B"

# FEATURES

source  
1..774  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2393463"  
/clone\_lib="NCI-CGAP Col6"  
/tissue\_type="colon tumor, RER+"  
/lab\_host="DH10B"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP\_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloned IDs 1057416-1061255, and 114584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 153 a 220 c 221 g 179 t 1 others  
ORIGIN

# alignment\_scores:

Quality: 399.00 Length: 117  
Ratio: 4.200 Gaps: 2  
Percent Similarity: 81.197 Percent Identity: 74.359

# alignment\_block:

US-09-016-869A-4 x AI765096/rev ..

Align seg 1/1 to reverse of: AI765096 from: 1 to: 774

```

22 AlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyAlaAs 38
|||||
677 GCGCCAGGGGGGGCCCCCGCTGTGGGCCATCGTGTATGCTATTGAGGA 628
|||||
38 pProAsn.....GlyValAsnArgPheGlyArgAlaIleGlnValM 53
|||||
627 GCCAGCGTTTAGGCGCAGCAGCGCTTC.....CTAGAAGACCAGGTCA 584
|||||
53 etMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAla 69
|||||
583 TGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGCGCGG 534
|||||
70 GluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAl 86
|||||
533 GAGCCCAATTGGCGCGACCCGCCCACTTTCACCCGACCGTGCACGACGC 484
|||||
86 aAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyA 103
|||||
483 TGCCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGCACCGGCGGG 434
|||||
103 laArgLeuAspValArgAspAlaThrGlyArgLeuProValAspLeuAla 119
|||||
433 CGCGCTGACGCTGCGCAATGCTGGGCGCGTCTGCCGTGGACCTGGCT 384
|||||
120 GluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGl 136
|||||
383 GAGGAGCTGGGCGCATCGCATGTCCCGGTTACCTGCGCGGCTTCGGG 334
|||||
136 Y 136
333 G 333

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seq\_name: gb\_gss7:AQ496105

# seq\_documentation\_block:

LOCUS AQ496105 614 bp DNA GSS 28-APR-1999  
DEFINITION HS.5075.A1.F12.T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-651 Col-23 Row-K, genomic survey sequence.

ACCESSION AQ496105

VERSION AQ496105.1 GI:4696228

# KEYWORDS

GSS.

# SOURCE

human.

# ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 614)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

COMMENT On Dec 15, 1999 this sequence version replaced gi:4575297. Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 651 row: K column: 23 Seq primer: 17 Class: BAC ends High quality sequence stop: 614. Location/Qualifiers

FEATURES

Source

1..614

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="Plate=651 Col=23 Row=K"

/clone\_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBAC3.6; Site.1: EcoRI; Site.2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT 117 a 182 c 171 g 133 t 11 others

ORIGIN

alignment\_scores

Quality: 391.00 Length: 86

Ratio: 4.827 Gaps: 0

Percent Similarity: 94.186 Percent Identity: 89.535

alignment\_block:

US-09-016-869A-4 x A0496105 ..

Align seg 1/1 to: A0496105 from: 1 to: 614

51 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 67

291 CAAGTCATGATGATGGCACCGCCGCGAGTGGCGAGCTGCTGCTCCA 340

67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84

341 CGGGGGGGAGCCCACTGCGCCGACCCCGCCACTCTCACCCAGCCGTGC 390

84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100

391 ACGACGCTGCCGGGAGGGTCTCTGACACACTGGTGTGTCGACCGG 440

101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117

441 GCCGGGGCGGCTGGACGTGCTGATGCTGGGGCGCTCTGCCGTGGA 490

117 pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134

491 CTGGCTGAGGAGCTGGGCATCTCGATGTTACCGGTACCTGCGCGCG 540

134 laThrGly 136

541 ATCGGGG 548

seq\_name: gb\_est19:AI363262

## seq\_documentation\_block:

LOCUS AI363262 708 bp mRNA EST 16-FEB-1999

DEFINITION qv56f03.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3' similar to TR:Q13195 Q13195 P16INK4/WTSL [2] TR:Q13399 ; contains UTR9.b3 TAR1 repetitive element ; , mRNA sequence.

ACCESSION AI363262

VERSION AI363262.1 GI:4114883

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 708)

## REFERENCE

AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index

UNPUBLISHED (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 872 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 394.

Location/Qualifiers

1..708

Source

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2016029"

/clone\_lib="NCI\_CGAP\_Brn23"

/tissue\_type="glioblastoma (pooled)"

/lab\_host="DH103"

/note="organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 137 a 210 c 219 g 140 t 2 others

ORIGIN

## alignment\_scores:

Quality: 390.00 Length: 96

Ratio: 4.588 Gaps: 1

Percent Similarity: 88.542 Percent Identity: 83.333

## alignment\_block:

US-09-016-869A-4 x AI363262/rev ..

Align seg 1/1 to reverse of: AI363262 from: 1 to: 708

41 GlyValAsnArgPheGlyArgArgAlaIleGlnValMetMetGlyse 57

|||||:::|||||

564 GGCAGCAGCCGCTTC.....CTAGAAGANCAGGTCAATGATGATGCAAG 521

57 rAlaArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysA 74

|||||:::|||||

520 CGCCCGAGTGGCGAGCTGCTGCTCCCGGGCGGAGCCCACTGCG 471



```
74 laaspProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGly 90
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
470 ACGACCCGCCCAACTCTCACCGACCGGTCACGAGCTGCCGCGGAGGC 421
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
91 PheLeuAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspVa 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
420 TTCCTGGACAGCTGGTGGTCTGCACCGCGCGCGCGCGCTGGACGT 371
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
107 lArgAspAlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyH 124
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
370 GCGCGATGCTGGGCGCGCTCTGCCGTGGACCTGGCTGAGGAGTGGGCC 321
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
124 lArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
320 ATCCGATGTCGACGGTACCTGCGCGCGCTGCGGG 283
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

seq\_name: gb\_est25:A1817709

seq\_documentation\_block: 729 bp mRNA EST 21-DEC-1999  
LOCUS A1817709  
DEFINITION WK25cl1.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA sequence.

ACCESSION A1817709  
VERSION A1817709.1 GI:5436788  
KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index

JOURNAL

COMMENT Unpublished (1998)

On Apr 7, 1998 this sequence version replaced gi:3035534.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Insert Length: 848 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 468.

Location/Qualifiers

FEATURES

SOURCE

1..729

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="NCI\_CGAP\_Brn25"

/tissue\_type="anaplastic oligodendroglioma"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; lstr

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGGAGCGCGCGCATAGTGTGTGTGTGTGTGTGT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

141 a 214 c 226 g 143 t 5 others

BASE COUNT

ORIGIN

alignment\_scores:  
Quality: 384.00 Length: 127  
Ratio: 3.959 Gaps: 2  
Percent Similarity: 76.378 Percent Identity: 69.291  
alignment\_block:  
US-09-016-869a-4 x A1817709/rev ..

Align seg 1/1 to reverse of: A1817709 from: 1 to: 729

32 SetTrpGluAlaGlyAlaAspProAsnGlyVal...AsnArgPheGlyAr 47  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

677 TCGTGGTTCACATCCCGGNGCTCACGGGAGTGGGCGAGCCAGGGGCG 628  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

47 gArgAlaIle..... 50  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

627 CCGCGNGCTGTGGCCCTCGTCTACTGAGAGCCAGCGCTAGG 578  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

51 .....GlnValMetMetMetGlySerAlaArg 59  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

577 GCAGCAGCCGCTCTCTAGAGACCGAGTCTATGATGAT.GGCAGCGCCGAA 529  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

60 ValAlaGluLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

528 GTGGCGGAGCTGCTGCTCCACGGCGCGGAGCCCACTGCGCCGACNC 479  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeu 93  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

478 CGCCACCTCTCACCGACCCCTGCACGACGCTGCCCGGAGGCTTCCTGG 429  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArg 109  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

428 ACACGCTGGTGGTCTCACCGCGCGGCGGCTGGACGTGCGCGAT 379  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

378 GCTTGGGCGCGCTGCTGCCGTGGACCTGCTGAGGAGCTGGCCCATCGCA 329  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

126 pValAlaGlyTyrLeuArgThrAlaThrGly 136  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

328 TGTGCGACGGTACCTGCGCGCGGCTGCGGG 298  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

seq\_name: gb\_est27:A1954684

seq\_documentation\_block: 563 bp mRNA EST 08-MAR-2000

LOCUS A1954684

DEFINITION wq34h12.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:247323 3' similar to SW:CDN2\_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR

A ;, mRNA sequence.

ACCESSION A1954684

VERSION A1954684.1 GI:5746994

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 563)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Insert Length: 613 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 460.  
Location/Qualifiers

## FEATURES

source

1. .563  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2473223"  
/clone\_lib="NCI\_CGAP\_GC6"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI\_CGAP\_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 112 a 158 c 169 g 124 t

ORIGIN

## alignment\_scores:

Quality: 381.00 Length: 90  
Ratio: 4.590 Gaps: 0  
Percent Similarity: 92.222 Percent Identity: 88.889

## alignment\_block:

US-09-016-869A-4 x AI954684/rev ..

Align seg 1/1 to reverse of: AI954684 from: 1 to: 563

47 ArgArgAlaileInValMetMetMetGlySerAlaArgValAlaGluLe 63  
|||||  
::: |||||||  
563 AGGCCAAATGTAGGGTCATGATGATGGCAGCGCCGAGTGGCGGAGCT 514  
63 uLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThrLeu 80  
|||||  
|||||  
513 GCTGCTGTCTCCACGGCGGGAGGCCCACTG.CCCGACCCGCCCACTCTCA 465  
80 hrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThrLeuVal 96  
|||||  
|||||  
464 CCCGACCCGTGCACACGCTGCCGGAGGGCTCTCTGGACACGCTGGT 415  
97 ValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyAr 113  
|||||  
|||||  
414 GTGCTGCACCGCGCGGGCGGGCTGGACGTGCGCGATGCTGGGGCGG 365  
113 gLeuProValAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyT 130  
|||||  
|||||  
364 TCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGCGCACGCT 315  
130 yLeuArgThrAlaThrGly 136  
|||||  
|||||  
314 ACCTGCGCGGCTGCGGGG 295

seq\_name: gb\_est26:AI885362

## seq\_documentation\_block:

LOCUS AI885362 528 bp mRNA EST 07-MAR-2000  
DEFINITION w192h04.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2432407 3'  
similar to SW:CDN2\_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR  
A.; mRNA sequence.

ACCESSION AI885362

VERSION AI885362.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 528)

## AUTHORS

TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTIGAP), Tumor Gene Index

## JOURNAL

COMMENT

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert\_Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 626 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 465.

Location/Qualifiers

source

1. .528

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2432407"

/clone\_lib="NCI\_CGAP\_Brn25"

/tissue\_type="anaplastic oligodendroglioma"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site1: Not I; Site2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGCGCGCATAGCTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 106 a 143 c 165 g 114 t

ORIGIN

## alignment\_scores:

Quality: 377.00 Length: 77  
Ratio: 5.027 Gaps: 0  
Percent Similarity: 97.403 Percent Identity: 94.805

## alignment\_block:

US-09-016-869A-4 x AI885362/rev ..

Align seg 1/1 to reverse of: AI885362 from: 1 to: 528

60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76  
|||||  
|||||  
528 GTGCGGAGCTGCTGCTGCTCCACGCGCGGAGCCCACTGCGCGACCC 479  
76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA 93  
|||||  
|||||  
478 CGCCACTCTCACCCGACCGGTGCACGACGCTGCCGGGAGGGCTTCCTGG 429  
93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109  
|||||  
|||||  
428 ACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 379  
110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126  
|||||  
|||||  
378 GCTGGGGCGGCTGCGCCCTGGACCTGGCTGGAGAGCTGGGGCATCGCA 329  
126 pValAlaGlyTyrLeuArgThrAlaThrGly 136  
|||||  
|||||  
328 TGTCGCACGCTACCTGCGCGGCTGCGGGG 298

seq\_name: gb\_est23:AI633790

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seq_documentation_block: 531 bp mRNA EST 14-DEC-1999
LOCUS AI633790
DEFINITION tt28610.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242122 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI633790
VERSION AI633790.1 GI:4685120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 531)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI_CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 623 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 454.
Location/Qualifiers
source
1. .531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2242122"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 107 a 144 c 163 g 116 t 1 others
ORIGIN

alignment_scores:
Quality: 373.00 Length: 78
Ratio: 4.973 Gaps: 0
Percent Similarity: 96.154 Percent Identity: 93.590

alignment_block:
US-09-016-869A-4 x AI633790/rev ..
Align seg 1/1 to reverse of: AI633790 from: 1 to: 531

59 ArgValAlaGluLeuLeuHisGlyAlaGluProAsnCysAlaAs 75
|||||
531 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGCCCACTGCGCGCA 482
|||||
75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 92
|||||
481 CNCCGCCACTCTCACCCACCGCTGCACGACGCTGCCCGGGAGGCTTCC 432
|||||
92 euAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArg 108
|||||
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```
431 TGGACACGCTGCTGCTGCACCGGGCGGCGGCTGCGCTGCGGC 382
109 AsplaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyHisAr 125
|||||
381 GATGCTGGGGCCGCTGCTGCGGTGACCTGCTGAGGAGCTGGGCCATCG 332
|||||
125 gAspValAlaGlyTyrLeuArgThrAlaThrGly 136
|||||
331 CGATGTGCGACGGTACCTGCGCGGCTGCGGG 298
|||||

seq_name: gb_est23:AI638416

seq_documentation_block: 528 bp mRNA EST 14-DEC-1999
LOCUS AI638416
DEFINITION tt31903.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI638416
VERSION AI638416.1 GI:4690650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI_CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 462.
Location/Qualifiers
source
1. .528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2242420"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 163 g 114 t 2 others
ORIGIN

alignment_scores:
Quality: 369.00 Length: 78
Ratio: 4.920 Gaps: 0
Percent Similarity: 96.154 Percent Identity: 92.308

alignment_block:
US-09-016-869A-4 x AI638416/rev ..
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Align seg 1/1 to reverse of: A1638416 from: 1 to: 528

59 ArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAs 75  
 |||||  
 528 CGAGTGGCGAGCTGTGCTGCCAGCGCGGAGCCCAACTGCGNCGA 479  
 |||||  
 75 pProAlaThrLeuThrArgProValHisaspAlaAlaArgGluGlyPheL 92  
 |||||  
 478 CNGCGCACTCTCACCGACCGCTGACGACGCTGCCGGGAGGCTTCC 429  
 |||||  
 92 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 108  
 |||||  
 428 TGGACAGCTGGTGGTGTCTCACCGCGCGCGGCGGCTGGAGCTGCCG 379  
 |||||  
 109 AspAlaTrpGlyArgLeuProValAspLeuAlaGluGlyHisAr 125  
 |||||  
 378 GATGCTGGGGCGCTGTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 329  
 |||||  
 125 gAspValAlaGlyTyrLeuArgThrAlaThrGly 136  
 |||||  
 328 CGATGTGCGACGCTACCTGCGCGCGCTGCGGGG 295

seq\_name: gb\_est13:AA909181

seq\_documentation\_block: 526 bp mRNA EST 10-JUN-1998  
 LOCUS AA909181  
 DEFINITION O112b04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:1523215 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE  
 REGULATOR BETA FORM ;, mRNA sequence.  
 ACCESSION AA909181  
 VERSION AA909181.1 GI:3048586  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 526)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Apr 7, 1998 this sequence version replaced gi:3034533.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LILN; contact the  
 IMAGE Consortium ([info@image.liln.gov](mailto:info@image.liln.gov)) for further information.  
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 /note="Organ: pooled; Vector: pT7A3D-Pac (Pharmacia) with  
 a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBHL19W, testis NHT, and B-cell  
 NCI-CGAP-GCB1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 882632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

FEATURES  
 source

BASE COUNT 82 a 175 c 155 g 113 t 1 others  
 ORIGIN

alignment\_scores:  
 Quality: 351.00 Length: 86  
 Ratio: 4.500 Gaps: 1  
 Percent Similarity: 90.698 Percent Identity: 88.372

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 464 GCGCGGAGCCCAACTGCGCGGAGAGAGAGAGAGAGAGAGAGAG 415  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:05:24 ; Search time 2513.97 Seconds  
(without alignments)  
605.555 Million cell updates/sec

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Perfect score: 853  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database :

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4: gb\_ov: \*

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9: gb\_pr1: \*

10: gb\_pr2: \*

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15: gb\_un: \*

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79: gb\_htg30: \*  
80: gb\_htg31: \*  
81: gb\_v11: \*  
82: gb\_v12: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
1	674.4	79.1	713	12	MUSARF	L76092 Mus musculus	
2	674.4	79.1	713	12	S80650	S80650 p16INK4a-CD	
3	672.8	78.9	713	5	I89920	I89920 Sequence 1	
4	640	75.0	846	12	MUSP16INK	L76150 Mus musculus	
5	640	75.0	849	12	AF044336	AF044336 Mus muscu	
6	638.4	74.8	849	12	AF044335	AF044335 Mus muscu	
7	382.2	44.8	507	5	AR062814	AR062814 Sequence	
8	375	44.0	395	5	AR001335	AR001335 Sequence	
9	375	44.0	395	5	AR037515	AR037515 Sequence	
10	375	44.0	395	5	AR062795	AR062795 Sequence	
11	375	44.0	395	5	I41169	I41169 Sequence 25	
12	345	40.4	482	12	MMINK4A02	U66087 Mus musculus	
13	339	39.7	339	12	MSU79634	U79634 Mus spretus	
14	335.8	39.4	339	12	MMU79632	U79632 Mus musculus	
15	335.8	39.4	339	12	MMU79633	U79633 Mus musculus	
16	334.2	39.2	339	12	MMU79630	U79630 Mus musculus	
17	332.6	39.0	339	12	MMU79631	U79631 Mus musculus	
18	319.8	37.5	336	12	MMU79635	U79635 Mus musculus	
19	267	31.3	707	12	L81167	L81167 Rattus norv	
20	229.2	26.9	1017	10	HSU26727	U26727 Human p16IN	
21	228.8	26.8	660	11	S78535	S78535 tumor suppr	
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24	224.4	26.3	1131	5	AR001325	AR001325 Sequence	

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29	208.6	24.5	540	5	I89921	I89921 Sequence 3
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## ALIGNMENTS

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LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
MEDLINE		
FEATURES		

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DEFINITION	p16INK4a=CDK4 and CDK6 cyclin D-dependent kinases inhibitor [alternative] spliced, exon 1 beta and exon 2 [mice, MEL erythroleukemia cells, mRNA Partial, 713 nt].			
ACCESSION	S80650			
VERSION	S80650			
KEYWORDS	S80650.1	GI:1245977		
SOURCE	Mus sp. MEL erythroleukemia cells.			
ORGANISM	Mus sp.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 713)			
TITLE	Alternative reading frames of the INK4a tumor suppressor gene			
JOURNAL	encode two unrelated proteins capable of inducing cell cycle			
MEDLINE	Cell 83 (6), 993-1000 (1995)			
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbs 174807] from the original journal article.			
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ORIGIN

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QY 61 GGGCCGCCACCTCCAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAG 120  
DB 84 GGGCCGCCACCTCCAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAG 143  
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189920 713 bp DNA PAT 10-AUG-1998  
LOCUS

DEFINITION Sequence 1 from patent US 5723313.  
ACCESSION 189920  
VERSION 189920.1 GI:3409860  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 713)  
AUTHORS Sherr,C.J. and Quelle,D.E.  
TITLE ARF-p19, a novel regulator of the mammalian cell cycle  
JOURNAL Patent: US 5723313-A 1 03-MAR-1998;  
FEATURES Location/Qualifiers  
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DB 684 TTAATAAATACATAAATGCTTTTTT 711  
RESULT 4  
MUSP16INK

LOCUS MUSP16INK 846 bp mRNA ROD 20-JAN-1996  
DEFINITION Mus musculus CDK4 and CDK6 inhibitor protein (p16ink4a) mRNA, complete cds.  
ACCESSION L76150  
VERSION L76150.1 GI:1162948  
KEYWORDS CDK4 inhibitor; CDK6 inhibitor.  
SOURCE Mus musculus cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 846)  
AUTHORS Quelle, D.E., Ashmun, R.A., Hannon, G.J., Rehberger, P.A., Trono, D., Richter, K.H., Walker, C., Beach, D., Sherr, C.J. and Serrano, M.  
TITLE Cloning and characterization of murine p16INK4a and p15INK4b genes  
JOURNAL Oncogene 11 (4), 635-645 (1995)  
MEDLINE 95380169  
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Db 191 GTACCCGATTCAGGTGATGATGGCAAGTTCAGGTACAGCTCTCTGCTCAACT 250  
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RESULT 5  
LOCUS AF044336 849 bp mRNA ROD 01-APR-1998  
DEFINITION Mus musculus strain DBA/2N cyclin dependent kinase inhibitor p16INK4a (Cdkn2a) mRNA, complete cds.  
ACCESSION AF044336  
VERSION AF044336.1 GI:3002948  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 849)  
AUTHORS Zhang, S., Ramsay, E.S. and Mock, B.A.  
TITLE Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a) and p19(ARF), is a candidate for the plasmacytoma susceptibility locus, pcdrl  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)  
MEDLINE 98151529  
REFERENCE 2 (bases 1 to 849)  
AUTHORS Zhang, S., Ramsay, E.S. and Mock, B.A.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-1998) NCI/NIH, 37 Convent Dr., Bethesda, MD 20892, USA  
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Qy 196 GAATCCTGGACAGGTGATGATGGCAAGTTCAGGTACAGCTCTCTGCTCAACT 255  
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Db 401 GTGCCCCACGACGCGGATAGCTTCAGCTCAAGCACGCCCGCAGG 445

RESULT 13  
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DEFINITION Mus spretus cyclin-dependent kinase inhibitor protein (p16(INK4a))  
ACCESSION U79634  
VERSION U79634.1 GI:4098165  
KEYWORDS western wild mouse.  
SOURCE Mus spretus  
ORGANISM Mus spretus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,  
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.  
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
JOURNAL Unpublished  
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,  
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.

Direct Submission  
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,  
Cantoblanco, Madrid, Madrid 28049, Spain  
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Db 301 GCCCAGACCGGCGCATAGCTTCAGCTCAAGCACGCCCGC 339

RESULT 14  
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DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))  
ACCESSION U79632  
VERSION U79632.1 GI:4098151  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,  
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.  
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

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JOURNAL      in mouse inbred strains
REFERENCE    Unpublished
AUTHORS      Santos.J., Melendez.B., Perez de Castro.I., Malumbres.M.,
              Serrano.M., Pellicer.A. and Fernandez-Piqueras.J.
TITLE        Direct Submission
JOURNAL      Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
              Cantoblanco, Madrid, Madrid 28049, Spain
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Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 270 AACTGCGAGGACCCCACTACTCTCCGCCGGTGCAGGCGTCCAGCAGCGCGGGAGGCTTC 329
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QY 330 CTGGACACGCTGTGTGCTGCACGGGCTCGGCTGGATGTGCGCGATGCCTGG 389
DB 121 CTGGACACGCTGTGTGCTGCACGGGCTCGGCTGGATGTGCGCGATGCCTGG 180
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DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (pl6(INK4a))
ACCESSION U79633
VERSION   U79633.1 GI:4098153
KEYWORDS  house mouse.
SOURCE    Mus musculus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
Santos.J., Melendez.B., Perez de Castro.I., Malumbres.M.,
Serrano.M., Pellicer.A. and Fernandez-Piqueras.J.
Comparative analysis of the pl6(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
Unpublished
2 (bases 1 to 339)
Santos.J., Melendez.B., Perez de Castro.I., Malumbres.M.,
Serrano.M., Pellicer.A. and Fernandez-Piqueras.J.
Direct Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
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BASE COUNT   54 a 101 c 111 g 73 t
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Query Match   39.4%; Score 335.8; DB 12; Length 339;
Best Local Similarity 99.4%; Pred. NO. 4e-76;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 210 GTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCGATTCG 269
DB 1 GTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCGATTCG 60
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QY 330 CTGGACACGCTGTGTGCTGCACGGGCTCGGCTGGATGTGCGCGATGCCTGG 389
DB 121 CTGGACACGCTGTGTGCTGCACGGGCTCGGCTGGATGTGCGCGATGCCTGG 180
QY 390 GGTCCGCTGCGGCTCGACTTGGCCCCAAGAGCGGGGACATCAAGACATCGTGCATATTG 449
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DB 301 GCCCAGACCGACGGGATAGCTTCAGCTCAAGCAGCGCC 339

Search completed: July 21, 2000, 06:05:30
Job time: 14864 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:18:48 ; Search time 107.17 Seconds  
(without alignments)  
1991.358 Million cell updates/sec

Title: US-09-016-869A-5  
Perfect score: 853  
Sequence: 1 GGACTACAGCGCGGAGCA.....GATACCTTTTAAATGTCAA 853

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	674.4	79.1	713	1 T62485	Murine ARF-p19 CDN
3	382.2	44.8	507	1 V70623	Mouse multiple tum
4	375	44.0	395	1 V11259	Mouse p16 CDNA fra
5	375	44.0	395	1 V53840	Nucleotide sequenc
6	375	44.0	395	1 V70604	CDNA encoding a mu
7	226	26.5	1131	1 V70594	CDNA encoding a hu
8	224.4	26.3	1131	1 T00744	Multiple tumour su
9	224.4	26.3	1131	1 Q99164	Human MTS1 polypept
10	224.4	26.3	1131	1 T69780	Human multiple tum
11	224.4	26.3	1131	1 V11249	Human MTS1E1-beta
12	224.4	26.3	1131	1 V53830	Coding sequence 1
13	208.6	24.5	540	1 T62486	Human ARF-p19 CDNA
14	162.4	19.0	393	1 V70624	Mouse multiple tum
15	159.2	18.7	447	1 T00736	Multiple tumour su
16	159.2	18.7	447	1 Q99158	Human multiple tum
17	159.2	18.7	471	1 V11238	Human MTS1 CDNA. D
18	159.2	18.7	471	1 V53819	Nucleotide sequenc
19	159.2	18.7	471	1 V70583	CDNA encoding a hu
20	159.2	18.7	737	1 X26233	Truncated p27/p16
21	159.2	18.7	782	1 X26234	Truncated p27/p16
22	159.2	18.7	947	1 T00747	Multiple tumour su
23	159.2	18.7	947	1 T72311	Human multiple tum
24	159.2	18.7	947	1 V11270	Human MTS1 CDNA va
25	159.2	18.7	947	1 V53851	Coding sequence 3
26	159.2	18.7	947	1 V70615	CDNA encoding a hu
27	159.2	18.7	948	1 Q63491	Inhibitor of cyclin
28	159.2	18.7	987	1 T60951	Tumour suppressor
29	159.2	18.7	994	1 T02962	Cell-cycle regulat
30	159.2	18.7	1028	1 X26231	Truncated p27/p16
31	159.2	18.7	1073	1 X26232	Truncated p27/p16
32	159.2	18.7	1098	1 T74053	CDK inhibitory fus
33	159.2	18.7	1098	1 X26224	Human p16p27 fusio

## RESULT 1

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AC T02965;  
DT 01-MAR-1996 (first entry)  
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KW Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;  
KW CCR; gene therapy; transgenic animal; cancer; cell proliferation;  
KW ss; ds.  
OS Mus sp.  
FH Key  
FT cds  
FT Location/Qualifiers  
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PN W09528483-A1.  
PD 26-OCT-1995.  
PF 14-APR-1995; U04636.  
PR 14-APR-1994; US-227371.  
PR 25-MAY-1994; US-248812.  
PR 14-SEP-1994; US-306511.  
PR 29-NOV-1994; US-346147.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PI Beach DR, Demetrick DJ, Hannon GJ, Serrano M;  
DR WPI: 95-373798/48.  
DR P-PSDB: R85120.  
PT New cell cycle regulating proteins bind to cyclin dependent kinase -  
PT and related nucleic acids, antibodies etc., used in diagnosis and  
PT therapy of abnormal cell proliferation, degeneration etc.  
PS Example 4; Page 80; 109pp; English.  
CC cDNA (T02965) coding for the mouse cell-cycle regulatory (CCR)  
CC protein p13.5 (R85120) was isolated from an embryonal stem cell  
CC library using a probe based on human CCR p16 CDNA (T02962).  
CC The isolated cDNA can be used: to detect mutations in CCR  
CC genes that lead to cell proliferation; to breed transgenic  
CC animals to study cellular disorders involving CCR allele  
CC mutation/misexpression; and to correct CCR-deficient cells  
CC (gene therapy).  
SQ Sequence 853 BP; 192 A; 207 C; 274 G; 180 T;

## ALIGNMENTS

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35 159.2 18.7 1143 1 T74052 CDK inhibitory fus  
36 159.2 18.7 1143 1 X26223 Human p15(GS)p27 f  
37 159.2 18.7 1420 1 T74051 CDK inhibitory fus  
38 159.2 18.7 1420 1 X26220 Human p27-p16 fus1  
39 157.8 18.5 1187 1 T00739 Multiple tumour su  
40 157.8 18.5 1187 1 V11240 Human MTS1 genomic  
41 157.8 18.5 1187 1 V53821 Coding sequence 2  
42 157.8 18.5 1187 1 V70585 Human multiple tum  
43 157.6 18.5 447 1 T00749 Multiple tumour su  
44 157.6 18.5 447 1 T00750 Multiple tumour su  
45 157.6 18.5 471 1 T69768 Human multiple tum

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RESULT 2
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ID T62485 standard; cDNA; 713 BP.
AC T62485;
DE 16-AUG-1997 (first entry)
KW Murine ARF-p19 cDNA.
KW ARF-p19; alternative reading frame; cell cycle; cancer; diagnosis;
KW gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6;
KW inhibitor; ss.
OS Mus musculus.
FH Key
FT cds Location/Qualifiers
FT cds 43..552
FT cds /*tag= a
FT cds /product= ARF-p19
FT cds 236..613
FT cds /*tag= b
FT exon /product= INK4a-p16 C-terminal fragment
FT exon 1..232
FT exon /*tag= c
FT exon /note= "Exon 1-beta"
FT exon 233..702
FT exon /*tag= d
FT exon /note= "Exon 2"
FT primer_bind complement (56..75)
FT /*tag= e
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primer_bind /note= "5' primer for RT-PCR"
602..624
/*tag= f
primer_bind /note= "3' primer for RT-PCR"
W09712060-A1.
03-APR-1997. U15312.
25-SEP-1996; US-534975.
27-SEP-1995; US-534975.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PI Quelle DE, Sherr CJ;
DR WPI: 97-212919/19.
P-PSDB; W16321-22.
DR Nucleic acid encoding ARF-p19 which induces cell cycle arrest when
PT overexpressed - used for diagnosis and treatment of cancer, and for
PT drug screening
PS Claim 2; Fig 1; 49pp; English.
CC A murine cDNA molecule (T62485) homologous to human INK4A beta
CC transcripts (see also T62486) was isolated from a mouse
CC erythroleukaemia cell DNA library. Sequences of exon 1-beta are
CC spliced to exon 2 to create an open reading frame that encodes a
CC novel protein, ARF-p19 (W16321), which induces cell cycle arrest
CC when overexpressed. Unrelated sequences from exon 1-alpha (not
CC shown) are spliced to the same exon 2 acceptor site to open another
CC reading frame that encodes INK4a-p16 (C-terminal fragment given in
CC W16322), an inhibitor of the cyclin D-dependent kinases CDK4 and
CC CDK6. Economical reutilisation of protein coding sequences in this
CC manner is without precedent in mammalian genomes and the unitary
CC inheritance of INK4a-p16 and ARF-p19 may reflect a dual requirement
CC for both proteins in cell cycle control. ARF-p19 nucleic acids can
CC be used as probes or primers, or in gene therapy protocols to
CC induce cell arrest in eukaryotes or (antisense) to inhibit ARF-p19
CC activity, and to create transgenic animals useful as models for
CC cancer. Human ARF-p19 cDNA (T62486) has also been isolated.
SQ Sequence 713 BP; 133 A; 195 C; 223 G; 162 T;
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Query Match 79.1%; Score 674.4; DB 1; Length 713;
Best Local Similarity 99.7%; Pred. NO. 9.1e-184;
Matches 686; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 GAGGTACACGACGCGGAGCATGGTTCGAGAGTTCCTTGTGTCAGTGAAGGATTACGCGCGC 60
Db 24 GAGGTACACGACGCGGAGCATGGTTCGAGAGTTCCTTGTGTCAGTGAAGGATTACGCGCGC 83
Qy 61 GGGCGCGCCACTCCAAGAGAGGGTTTCTTGTGTAAGTTCGTGCGATCCCGAGAGACCAG 120
Db 84 GGGCGCGCCACTCCAAGAGAGGGTTTCTTGTGTAAGTTCGTGCGATCCCGAGAGACCAG 143
Qy 121 GACAGGAGCTCGGCTCTGGCTTTCGTGAAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 180
Db 144 GACAGGAGCTCGGCTCTGGCTTTCGTGAAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 203
Qy 181 AAGAGGGCGCGACCGGAATCCCTGGACCAAGTGTATGATGGCAACCTTACGTAAGCAG 240
Db 204 AAGAGGGCGCGACCGGAATCCCTGGACCAAGTGTATGATGGCAACCTTACGTAAGCAG 263
Qy 241 CTCCTCTGCTCAACTACGCTGAGATTTCGAACTGGGAGGACCCCACTACCTTCTCCGCGC 300
Db 264 CTCCTCTGCTCAACTACGCTGAGATTTCGAACTGGGAGGACCCCACTACCTTCTCCGCGC 323
Qy 301 CGGTGCACGACGACGCGGGAAGGCTTCTGAGACACGCTGGTGGTGTGCTGACAGGGTCAG 360
Db 324 CGGTGCACGACGACGCGGGAAGGCTTCTGAGACACGCTGGTGGTGTGCTGACAGGGTCAG 383
Qy 361 GGGCTCGGCTGGATGTCGCGATGCTGGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 420
Db 384 GGGCTCGGCTGGATGTCGCGATGCTGGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 443
Qy 421 GGGGACATCAAGACATCGTGGATATTGCGTTCGCTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 444 GGGGACATCAAGACATCGTGGATATTGCGTTCGCTGGTGGTGGTGGTGGTGGTGGTGG 503
Qy 481 GGTGCTCTTTGTGTACCGCTGGGAACGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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Db 241 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 300
QY 374 TGTGGCGATGCTGGGTGCTGCTCGGCTCGACCTTGACCTTGCCCAAGAGCGGGGACATCAAGA 433
Db 301 TGTCCGCGATGCTGGGTGCTGCTCGGCTCGACCTTGCCCAAGAGCGGGGACATCAAGA 360
QY 434 CATCGTGCATATTTGGCGTTCGCGTGGGTGCTCTT 468
Db 361 CATCGTGCATATTTGGCGTTCGCGTGGGTGCTCTT 395

RESULT 5
V53840
ID V53840 standard; DNA; 395 BP.
AC V53840;
DT 04-DEC-1998 (first entry)
DE Nucleotide sequence of nucleic acid 6.
KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
KW somatic mutation; gene therapy; ds.
OS Homo sapiens.
PN US5801236-A.
PD 01-SEP-1998.
PF 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 98-494842/42.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Disclosure: Column 83-84; 73pp; English.
CC This is the nucleotide sequence of a nucleic acid used in the
CC method of the invention involving the use of the multiple tumour
CC suppressor (MTS) gene to diagnose and treat human cancers. The MTS
CC gene is useful in the diagnosis and prognosis of human cancer, e.g.
CC by standard nucleic hybridisation techniques, of patient samples.
CC The mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

Query Match 44.0%; Score 375; DB 1; Length 395;
Best Local Similarity 98.5%; Pred. No. 3.7e-98;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACGCG-AGCTGC 133
Db 1 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACGCGTAGCTGC 60
QY 134 GCTCTGGCTTTGCTGAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCCGAC 193
Db 61 GCTCTGGCTTTGCTGAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCCGAC 120
QY 194 CGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 253
Db 121 CGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAACCTGCGAGGACCCCACTACCTCTCCCGCCGCGTGCACGACGC 313
Db 181 CTACGGTGCAGATTCGAACCTGCGAGGACCCCACTACCTCTCCCGCCGCGTGCACGACGC 240
QY 314 GCTCTGGCTTTGCTGAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCCGAC 193
Db 61 GCTCTGGCTTTGCTGAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCCGAC 120
QY 194 CGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 253
Db 121 CGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAACCTGCGAGGACCCCACTACCTCTCCCGCCGCGTGCACGACGC 313
Db 181 CTACGGTGCAGATTCGAACCTGCGAGGACCCCACTACCTCTCCCGCCGCGTGCACGACGC 240
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QY 314 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 373
Db 241 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 300
QY 374 TGTGGCGATGCTGGGTGCTGCTCGGCTCGACCTTGCCCAAGAGCGGGGACATCAAGA 433
Db 301 TGTCCGCGATGCTGGGTGCTGCTCGGCTCGACCTTGCCCAAGAGCGGGGACATCAAGA 360
QY 434 CATCGTGCATATTTGGCGTTCGCGTGGGTGCTCTT 468
Db 361 CATCGTGCATATTTGGCGTTCGCGTGGGTGCTCTT 395

RESULT 6
V70604
ID V70604 standard; cDNA; 395 BP.
AC V70604;
DT 03-FEB-1999 (first entry)
DE cDNA encoding a murine multiple tumour suppressor lE1-beta protein.
KW Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Mus sp.
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI; 99-044585/04.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 8; Fig 14; 80pp; English.
CC The present sequence encodes murine multiple tumour suppressor lE1-beta
CC (MTS1E1-beta) protein. Primers designed from the gene can be used to
CC design primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

Query Match 44.0%; Score 375; DB 1; Length 395;
Best Local Similarity 98.5%; Pred. No. 3.7e-98;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACGCG-AGCTGC 133
Db 1 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACGCGTAGCTGC 60
QY 134 GCTCTGGCTTTGCTGAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCCGAC 193
Db 61 GCTCTGGCTTTGCTGAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCCGAC 120
QY 194 CGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 253
Db 121 CGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAACCTGCGAGGACCCCACTACCTCTCCCGCCGCGTGCACGACGC 313
Db 181 CTACGGTGCAGATTCGAACCTGCGAGGACCCCACTACCTCTCCCGCCGCGTGCACGACGC 240
QY 314 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 373
Db 241 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 300
QY 374 TGTGGCGATGCTGGGTGCTGCTCGGCTCGACCTTGCCCAAGAGCGGGGACATCAAGA 433
Db 301 TGTCCGCGATGCTGGGTGCTGCTCGGCTCGACCTTGCCCAAGAGCGGGGACATCAAGA 360
QY 434 CATCGTGCATATTTGGCGTTCGCGTGGGTGCTCTT 468
Db 361 CATCGTGCATATTTGGCGTTCGCGTGGGTGCTCTT 395
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RESULT 7
V70594
ID V70594 standard; cDNA: 1131 BP.
AC V70594;
DE 03-FEB-1999 (first entry)
KW Multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 338..655
FT CDS /tag= a
FT /product= MTS1E1-beta
FT
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI: 99-044585/04.
DR P-PSDB; W80525.
PT Mouse multiple tumour suppressor gene segment - useful for primer
  design
PS Example 8; Fig 12A-B; 80pp; English.
CC The present sequence encodes a human multiple tumour suppressor 1E1-beta
  (MTS1E1-beta) protein. Primers designed from the gene can be used to
  design primers to detect abnormalities i.e. polymorphisms which may
  predispose towards malignancies such as melanoma, leukaemia,
  astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
  thyroid, pancreas, uterus and kidneys.
CC
SQ Sequence 1131 BP; 231 A; 327 C; 344 G; 229 T;

Query Match 26.5%; Score 226; DB 1; Length 1131;
Best Local Similarity 69.9%; Pred. No. 2.7e-55;
Matches 320; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

QY 9 GCACGGGAGCATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGCGCGCC 68
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 GCGCGGAGAACATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGCGCGCC 190

QY 69 CACTCCAAGAGAGGTTTCTTGGTGAAGTTCTGTCATCCCGGGCTCAGCGGAGTGGCGAC 128
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 GCGCGGAGTGGGTTTCTGTTCAATCCCGGGCTCAGCGGAGTGGCGAC 250

QY 129 GCTGCGCTCTGGCTTTCGTGAACATGTTGTTAGGCTAGAGAGTCTTGAAGAGGGC 188
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 CAGGGCGCGCGCGCTGTCGCTGATGCTACTGAGGAGCCAGCGTCTAGGC 310

QY 189 CGCACCGGAATCCT---GGACCAAGTGTATGATGGCAACGTTACGTAGCAGCTCTT 245
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AGCAGCGCTTCTAGAACACCAAGTGTATGATGGCAACGTTACGTAGCAGCTCTG 370

QY 246 CTGCTCAACTACGGTTCAGATTCCGAATCGGAGAGCCCACTACCTTCTCCCGCGGTG 305
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 CTGCTCTCCACGGCGGAGCCCACTTCCCTGGACACGCTGTTGTTGCTGACCGCGG 430

QY 306 CAGACCGCAGCGGAGGCTTCTTGGACACGCTGTTGTTGCTGACCGGTGAGGGCT 365
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 CAGACCGCTCCCGGAGGCTTCTTGGACACGCTGTTGTTGCTGACCGCGGCGG 490

QY 366 CGGCTGATGCGCGATGCTGGGGTCCGCTCGCGCTCGACTTGGCCCAAGACGCGGGA 425
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 CGGCTGACCTGCGGATGCTGGGGCTGCTGCGGCTGACCTTGGCTGAGGAGCTGGC 550

QY 426 CATCAAGACATGTCGATATTTCGTTCCGCTGGGTG 463
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 551 CATCGCATGTCGACCGGTACCTGCGCGGCTGCGGG 588

RESULT 8
T00744
ID T00744 standard; cDNA: 1131 BP.
AC T00744;
DE 08-MAY-1996 (first entry)
KW Multiple tumour suppressor 1 exon 1 beta (MTS1E1beta) gene ORF.
KW Multiple tumour suppressor; MTS1E1beta; cancer; diagnosis; assay;
  predisposition; melanoma; leukaemia; lymphoma; prognosis;
  pancreas; breast; thyroid; open reading frame; ORF; exon 1; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 338..655
FT CDS /tag= a
FT /product= MTS1E1-beta
FT
PN W09525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227359.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PI (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI: 95-344626/44.
DR P-PSDB; R81700.
PT Detecting polymorphism associated with cancer pre-disposition - also
  DNA, vectors and host cells e.g. for gene or protein replacement
  therapy and drug screening
PS Example 7; Pages 100-101; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
  by detecting an alteration in the wild type multiple tumour
  suppressor (MTS) gene, using gene probes which hybridise to the
  MTS1E1beta gene ORF T00744 (which encodes R81700). The above assay
  can also be used in the diagnosis and prognosis of melanoma,
  lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.
CC
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 26.3%; Score 224.4; DB 1; Length 1131;
Best Local Similarity 69.7%; Pred. No. 7.8e-55;
Matches 319; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 9 GCACGGGAGCATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGCGCGCC 68
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 GCGCGGAGAACATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGCGCGCC 190

QY 69 CACTCCAAGAGAGGTTTCTTGGTGAAGTTCTGTCATCCCGGGCTCAGCGGAGTGGCGAC 128
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 GCGCGGAGTGGGTTTCTGTTCAATCCCGGGCTCAGCGGAGTGGCGAC 250

QY 129 GCTGCGCTCTGGCTTTCGTGAACATGTTGTTAGGCTAGAGAGTCTTGAAGAGGGC 188
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 CAGGGCGCGCGCGCTGTCGCTGATGCTACTGAGGAGCCAGCGTCTAGGC 310

QY 189 CGCACCGGAATCCT---GGACCAAGTGTATGATGGCAACGTTACGTAGCAGCTCTT 245
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AGCAGCGCTTCTAGAACACCAAGTGTATGATGGCAACGTTACGTAGCAGCTCTG 370

QY 246 CTGCTCAACTACGGTTCAGATTCCGAATCGGAGAGCCCACTACCTTCTCCCGCGGTG 305
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 CTGCTCTCCACGGCGGAGCCCACTTCCCTGGACACGCTGTTGTTGCTGACCGCGG 430

QY 306 CAGACCGCAGCGGAGGCTTCTTGGACACGCTGTTGTTGCTGACCGGTGAGGGCT 365
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 CAGACCGCTCCCGGAGGCTTCTTGGACACGCTGTTGTTGCTGACCGCGGCGG 490

QY 366 CGGCTGATGCGCGATGCTGGGGTCCGCTCGCGCTCGACTTGGCCCAAGACGCGGGA 425
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 CGGCTGACCTGCGGATGCTGGGGCTGCTGCGGCTGACCTTGGCTGAGGAGCTGGC 550

QY 426 CATCAAGACATGTCGATATTTCGTTCCGCTGGGTG 463
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 551 CATCGCATGTCGACCGGTACCTGCGCGGCTGCGGG 588
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RESULT 9
Q99164
ID Q99164 standard; cDNA; 1131 BP.
AC Q99164;
DE 03-MAY-1996 (first entry)
DE Human MTS polypeptide, MTS1E1-beta encoding cDNA.
KW Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW gene therapy; chronic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 338..655
FT /tag= a
FT /product= MTS1E1-beta
PN WO9525429-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03316.
PR 18-MAR-1994; US-214581.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215088.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 95-344401/44.
DR P-PSDB; R80947.
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
PT melanoma or leukaemia
PS Claim 4; Page 100-101; 156pp; English.
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC polypeptides have been isolated and sequenced. This sequence encodes
CC the MTS polypeptide MTS1E1-beta (R80947). MTS polypeptide-encoding cDNAs
CC and mutants of these are useful for the diagnosis or prognosis of
CC human cancer. Germ-line mutations of MTS cDNAs can be used for
CC diagnosing predisposition to melanoma, leukaemia, astrocytoma,
CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers
CC of the pancreas, thyroid, ovary, uterus, kidney, stomach and
CC rectum. The wild-type gene is useful for gene therapy and MTS
CC polypeptides may also be used for protein replacement therapy. Also
CC the polypeptides or cells contg. an altered MTS gene are useful for
CC screening for potential cancer therapeutics.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 26.3%; Score 224.4; DB 1; Length 1131;
Best Local Similarity 69.7%; Pred. No. 7.8e-55;
Matches 319; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 9 GCAGCGGAGCATGGTGCAGGTTCTTGGTCACTGTAAGGATTCAGCGCGGCGCGCC 68
DB 131 GCGGCGAGAACATGGTGCAGGTTCTGTTGACCTCCCGATTCGGCGCGGTGCGGAC 190
QY 69 CACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAGGACAGCGA 128
DB 191 CGCCCGAGTGAAGGTTTCTGTTGTTTACATCCCGCGGTACCGGGGAGTGGGCGAC 250
QY 129 GCTGGCTCTGGCTTTCGTGAACATGTTGTTGAGCTAGAGAGGATCTTGAGAGAGGGC 188
DB 251 CAGGGGCGCGCGCGCTGTGGCCCTCGTGTGATCTACTGAGGAGCCAGCGTCTAGGGC 310
QY 189 CGCACCGGAATCCT---GGACCAAGTATGATGGCAACGTTACAGTACAGCTCTT 245
DB 311 AGCAGCCGCTTCTTAGAGAGACCAAGTATGATGGCAGCGCCGCGAGTGGCGAGCTG 370
QY 246 CTGCTCAACTAGGTGCAGATTCGAATTCGAGAGACCCCACTACCTTCTCCGCGCGGTG 305
DB 371 CTGCTGCTCCACGCGGCGGAGCCCAACTGCGCGGACCCCGCACTCTCACCGACCGGTG 430
QY 306 CACGACGAGCGCGGAGAGGGCTTCTTGGACACAGCTGTTGCTGCACGGGTACGGGCT 365
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Db 191 GCCCGAGTGGGTTTCGTGTTTACATCCCGCGGCTACAGGGGAGTGGCGAGCAC 250
Qy 129 GCTGGCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGATCTTGAAGAAGGGC 188
Db 251 CAGGGGCGCCCGCTGTGGCCCTCTGCTGATGCTACTGAGAGCAGCGTCTAGGGC 310
Qy 189 CGCACCGGAATCCT--GGACCAAGTGATGATGATGGCAACGTTACGTAGAGCTCTT 245
Db 311 AGCAGCGCTTCTCTAGAAGACCAAGTCTATGATGATGGCAGCGCCGAGTGGCGAGCTG 370
Qy 246 CTGCTCACTACGTGTCAGATTCGAATCTGGAGGAGCCCACTACCTCTCCCGCCGGTG 305
Db 371 CTGCTGCTCCACGCGGGAGCCCAATGCGCGAGCCCGCCCACTCTCACCCGACCCGTG 430
Qy 306 CACGACGAGCGCGGAGGCTTCTTGACACGCTGTGTGTGTCACGGGTTCAGGGGCT 365
Db 431 CACGACGCTGCGCGGAGGCTTCTTGACACGCTGTGTGTGTCACGGGTTCAGGGGCT 490
Qy 366 CCGCTGATGTCGCGGATGCTGGGTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 425
Db 491 CCGCTGATGTCGCGGATGCTGGGTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 550
Qy 426 CATCAAGACATCGTGGCATTTTGGTTCGCTGGGTG 463
Db 551 CATCGCATGTCGACCGTACCTGCGCGGCTGCGGG 588

RESULT 13
T62486
ID T62486 standard; cDNA; 540 BP.
AC T62486;
DT 16-AUG-1997 (first entry)
DE Human ARF-p19 cDNA.
KW ARF-p19; alternative reading frame; cell cycle; cancer; diagnosis;
KW gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6;
KW inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 142..540
FT FT /*tag= a
FT FT /product= ARF-p19
FT FT 338..538
FT FT /*tag= b
FT FT /product= INK4a-p16 C-terminal fragment
FT FT W09712060-A1.
PN 03-APR-1997.
PD 25-SEP-1996; U15312.
PF 27-SEP-1995; US-534975.
PR (SUUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PI Quelle DE, Sherr CJ;
DR WPI; 97-212919/19.
DR P-PSDB; W16323-24.
PT Nucleic acid encoding ARF-p19 which induces cell cycle arrest when
PT overexpressed - used for diagnosis and treatment of cancer, and for
PT drug screening
PS Claim 2; Fig 7; 49pp; English.
CC A human cDNA molecule (T62486) corresponds to INK4a beta
CC transcripts and includes a reading frame coding for a novel protein
CC (W16323). designated ARF-p19, which induces cell cycle arrest when
CC overexpressed. This reading frame asymmetrically overlaps a second
CC reading frame that encodes INK4a-p16 (C-terminal region given in
CC W16324), an inhibitor of the cyclin D-dependent kinases CDK4 and
CC CDK6. Economical reutilization of protein coding sequences in this
CC manner is without precedent in mammalian genomes and the unitary
CC inheritance of INK4a-p16 and ARF-p19 may reflect a dual requirement
CC for both proteins in cell cycle control. ARF-p19 nucleic acids can
CC be used as probes or primers, esp. for cancer diagnosis, or in gene
CC therapy protocols to induce cell arrest in eukaryotes or (antisense)
CC to inhibit ARF-p19 activity, and to create transgenic animals useful
CC as models for cancer.
SQ Sequence 540 BP; 68 A; 173 C; 216 G; 83 T;
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Query Match 24.5%; Score 208.6; DB 1; Length 540;
Best Local Similarity 71.3%; Pred. No. 1.9e-50;
Matches 290; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

Qy 9 GCAGCGGAGAGTGGGTGCGAGGTTCTTGGTCACTGTAAGGATTCAGCGCGCGGGCGGCC 68
Db 131 GCGGGGAGAACATGTCGTCAGGTTCTTGGTGACCCCTCGGATTCGGCGCGCTGCGGCC 190
Qy 69 CACTCCAAAGAGAGGTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAGGACAGCA 128
Db 191 CCGCCCGAGTGAAGGTTTTCGTGGTTTCAATCCCGCGGCTCACGGGGAGTGGCAGCGC 250
Qy 129 GCTGCGCTCTGGCTTTCGTGAACATGTTTGGAGGCTAGAGAGGATCTTGAGAGAGGCG 188
Db 251 CAGGGGCGCCCGCTGTCGCCCTCGTGTGCTACTGAGGAGCCAGCGTCTAGGGC 310
Qy 189 CGCACCGGAATCCT--GGACCAAGTGATGATGATGGCAACGTTACGTAGAGCTCTT 245
Db 311 AGCAGCGCTTCTCTAGAAGACCAAGTCTATGATGATGGCAGCGCCGAGTGGCGAGCTG 370
Qy 246 CTGCTCAACTACGTGTCAGATTCGAATCTGGAGGAGCCCACTGCGCGGCTGCTGCGCT 305
Db 371 CTGCTGCTCCACGCGGAGGCTTCTTGACACGCTGTGTGTGTCACCGCCGCTCTCAC 430
Qy 306 CACGACGAGCGCGGAGGCTTCTTGACACGCTGTGTGTGTCACCGGCTCAGGGGCT 365
Db 431 CACGACGCTGCGCGGAGGCTTCTTGACACGCTGTGTGTGTCACCGGCTGCGCGGCG 490
Qy 366 CCGCTGATGTCGCGGATGCTGGGTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 412
Db 491 CCGCTGATGTCGCGGATGCTGGGTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 537

RESULT 14
W70624
ID W70624 standard; cDNA; 393 BP.
AC W70624;
DT 03-FEB-1999 (first entry)
DE Mouse multiple tumour suppressor 2 gene (MTS2) coding sequence.
KW Murine; multiple tumour suppressor 2 gene; MTS2; cancer; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 1..393
FT FT /*tag= a
FT FT 132..133
FT FT /*tag= b
FT FT /note= "splice site"
FT FT US5843756-A.
PN 01-DEC-1998.
PD 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI; 99-044585/04.
DR P-PSDB; W70823.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 7; Fig 18; 80pp; English.
CC The present sequence encodes mouse multiple tumour suppressor 2
CC (MTS2) gene. The MTS1 gene can be used to design primers to
CC detect abnormalities i.e. polymorphisms which may predispose
CC towards malignancies such as melanoma, leukaemia, astrocytoma,
CC lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
CC Sequence 393 BP; 69 A; 124 C; 141 G; 59 T;

Query Match 19.0%; Score 162.4; DB 1; Length 393;
Best Local Similarity 77.8%; Pred. No. 2.7e-37;
Matches 196; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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Qy	206	CCAGGTGATGATGATGGCAACGTTCCAGTAGAGCTCTTCTGCTCAACTACGTTGCAGA	265
Db	129	CCAGGTGATGATGATGGCAGCCGAGGTGGACAGACTGCTGCTCCACGGAGCAGA	188
Qy	266	TTCGAACTGCGAGGACCCCACTACCTTCTCCGCCGGTGCACGACGACGCGGGAAGG	325
Db	189	ACCCAACTGCGCGACCTGCCACCTTACCAGACCTGTGCAGACGCACTCGGGAAGG	248
Qy	326	CTTCTCTGGACACGCTGGTGTGTGTGACGGGTTCAGGGGTTCGGCTGGATGTGCGCGATGC	385
Db	249	CTTCTCTGGACACGCTTGTCTGTGTGACCGGGCAGGGGCGGCTGGATGTGTGTGACGC	308
Qy	386	CTGGGTTGCGCTCCGCTGCACATTGCCCAAGACGGGGACATCAAGACATCGTGCGATA	445
Db	309	CTGGGGCCGCTTCGCGGTAGACTTGGCTGNAAGACAGGGCCCGCTGACATTGCGAGGTA	368
Qy	446	TTTGGCTTCCGC	457
Db	369	CTGCACTGCTGC	380

RESULT	15
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T00736	
ID	T00736 standard; CDNA; 447 BP.
AC	T00736;
DE	08-MAY-1996 (first entry)
DT	Multiple tumour suppressor 1 (MTS1) gene ORF.
KW	Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW	predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW	pancreas; breast; thyroid; open reading frame; ORF; ds.
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	1..447
FT	/tag= a
PN	W09525813-Al.
PD	28-SEP-1995.
PF	17-MAR-1995; U03537.
PR	18-MAR-1994; US-214582.
PR	18-MAR-1994; US-215087.
PR	18-MAR-1994; US-215086.
PR	14-APR-1994; US-227369.
PR	01-JUN-1994; US-251938.
PA	(MYRI - ) MYRIAD GENETICS INC.
PA	(UTAH ) UNIV UTAH RES FOUND.
PI	Cannon-Albright LA, Kamb A, Skolnick MH;
DR	WFI; 95-344626/44.
DR	P-PSDB; R81701.
PT	Detecting polymorphism associated with cancer pre:disposition - also
PT	DNA, vectors and host cells e.g. for gene or protein replacement
PT	therapy and drug screening
PS	Example 8; Pages 91-92; 148pp; English.
CC	An individual can be diagnosed as having a predisposition to cancer
CC	by detecting an alteration in the wild type multiple tumour
CC	suppresser (MTS) gene, using gene probes which hybridise to the MTS1
CC	gene ORF T00736 (which encodes R81701) mutant sequences T00749/50.
CC	The above assay can also be used in the diagnosis and prognosis of
CC	melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
CC	cancers, etc.
SQ	Sequence 447 BP; 64 A; 147 C; 172 G; 64 T;

Qy	316	CGCGGGAGGCTTCTCTGGACACGCTGGTGGTGTGACGGGTTCAGGGGTTCGGCICGATG	375
Db	233	CCCGGAGGGCTTCTCTGGACACGCTGGTGGTGTGACCGGGCCGGCGCGGTGGACG	292
Qy	376	TGGCGATGCGTGGGTTCGGCTCCCGTTCGACTTGGCCCAAGACGGGGACACATCAAGACA	435
Db	293	TGCGCATGCTGGGGCGCTCTCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATG	352
Qy	436	TCGTGCGATATTTGGTTCCGCTGGGTG	463
Db	353	TCGCACGGTACCTCGCGCGCGCTCGCGG	380

Search completed: July 21, 2000, 06:18:54  
Job time: 13651 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:06:34 ; Search time 86.37 Seconds  
(without alignments)  
1358.517 Million cell updates/sec

Title: US-09-016-869A-5  
Sequence: 853  
1 GGAGTACGACGCGGAGCA.....GATACCTTTTAAATGTCAA 853

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/5C\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/5D\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/6\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	853	100.0	853	4	US-08-306-511A-5
2	853	100.0	853	4	US-08-893-274-5
3	853	100.0	853	5	US-08-581-918A-5
4	853	100.0	853	6	PCT-US95-04636-5
5	672.8	78.9	713	2	US-08-534-975-1
6	672.8	78.9	713	3	US-08-954-470-1
7	672.8	78.9	713	5	US-09-129-855A-1
8	642	75.3	857	4	US-08-627-610-5
9	382.2	44.8	507	3	US-08-508-735-44
10	375	44.0	395	1	US-08-474-177-25
11	375	44.0	395	2	US-08-487-033-25
12	375	44.0	395	2	US-08-480-810-25
13	375	44.0	395	3	US-08-508-735-25
14	375	44.0	395	4	US-08-848-251-25
15	375	44.0	395	4	US-08-486-047-25
16	375	44.0	395	5	US-09-120-130-25
17	375	44.0	395	5	US-09-115-252-25
18	226	26.5	1131	3	US-08-508-735-13
19	224.4	26.3	1131	1	US-08-474-177-13
20	224.4	26.3	1131	2	US-08-487-033-13
21	224.4	26.3	1131	4	US-08-480-810-13
22	224.4	26.3	1131	4	US-08-848-251-13
23	224.4	26.3	1131	4	US-08-486-047-13
24	224.4	26.3	1131	5	US-09-120-130-13
25	224.4	26.3	1131	5	US-09-115-252-13
26	208.6	24.5	540	2	US-08-534-975-3

## ALIGNMENTS

RESULT 1  
US-08-306-511A-5  
; Sequence 5, Application US/08306511A  
; Patent No. 5962316  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannan, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,511A  
; FILING DATE: 14-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 853 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 213..587  
; US-08-306-511A-5  
  
Query Match 100.0% Score 853; DB 4; Length 853;  
Best Local Similarity 100.0%; Pred. No. 2.1e-239;

Matches 853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGTACAGCAGCGGAGCATGGTGCAGGTTCTTGTCACCTGTAAGGATTCAGCGGC 60  
DB 1 GGAGTACAGCAGCGGAGCATGGTGCAGGTTCTTGTCACCTGTAAGGATTCAGCGGC 60

QY 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGTTGAAGTTCGTGCGATCCCGGAGACCCAG 120  
DB 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGTTGAAGTTCGTGCGATCCCGGAGACCCAG 120

QY 121 GACACGAGCTCGCTCTGGTCTTCTGTCACATGTTGTAGGCTAGAGAGATCTTGAG 180  
DB 121 GACACGAGCTCGCTCTGGTCTTCTGTCACATGTTGTAGGCTAGAGAGATCTTGAG 180

QY 181 AAGAGGGCCGACCGGAACTCTGGACCAAGTGTATGATGGGCAAGTTCACGTAGCAG 240  
DB 181 AAGAGGGCCGACCGGAACTCTGGACCAAGTGTATGATGGGCAAGTTCACGTAGCAG 240

QY 241 CTCCTCTGCTCAACTACGCTGAGTTCGAATTCGAATTCGAGGAGCCCACTACCTTCTCCGCC 300  
DB 241 CTCCTCTGCTCAACTACGCTGAGTTCGAATTCGAATTCGAGGAGCCCACTACCTTCTCCGCC 300

QY 301 CGGTGACGAGCAGCGGAGGAGTTCCTGGACACGCTGGTGGTGTGTCACGCGGTGAG 360  
DB 301 CGGTGACGAGCAGCGGAGGAGTTCCTGGACACGCTGGTGGTGTGTCACGCGGTGAG 360

QY 361 GGGCTCGCTGATGTGCGGATGCTGGGTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420  
DB 361 GGGCTCGCTGATGTGCGGATGCTGGGTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420

QY 421 GGGGACATCAAGACATGCTGATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 GGGGACATCAAGACATGCTGATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 481 GGTGCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 540  
DB 481 GGTGCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 540

QY 541 GCACGCCAGCGGCGCTGGAATCTCGCGGCAATCCCAAGAGCAGAGTAAATCCGCGCTCA 600  
DB 541 GCACGCCAGCGGCGCTGGAATCTCGCGGCAATCCCAAGAGCAGAGTAAATCCGCGCTCA 600

QY 601 GCGCGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 660  
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QY 661 TAAAAATACATAATAATGCTTTTTCATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
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QY 721 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
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QY 781 GAAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
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QY 841 TTTAAATGTCAA 853  
DB 841 TTTAAATGTCAA 853

RESULT 2

US-08-893-274-5  
; Sequence 5, Application US/08893274  
; Patent No. 5968821  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,

TITLE OF INVENTION: and Uses Related Thereto  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,274  
FILING DATE: 15-JULY-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APRIL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOVEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DECEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,308  
FILING DATE: 16-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.09  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 853 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 213..587  
US-08-893-274-5

Query Match 100.0%; Score 853; DB 4; Length 853;  
Best Local Similarity 100.0%; Pred. No. 2.1e-239;  
Matches 853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGTACAGCAGCGGAGCATGGTGCAGGTTCTTGTCACCTGTAAGGATTCAGCGGC 60  
DB 1 GGAGTACAGCAGCGGAGCATGGTGCAGGTTCTTGTCACCTGTAAGGATTCAGCGGC 60

QY 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGTTGAAGTTCGTGCGATCCCGGAGACCCAG 120  
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QY 181 AAGAGGGCCGACCGGAACTCTGGACCAAGTGTATGATGGGCAAGTTCACGTAGCAG 240

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Db 181 AGAGGGCCGACCGGAATCTGGACAGGTGATGATGGCAACGTTACGTAGCAG 240  
QY 241 CTCCTTCTGCTCAACTACGGTGCAGATTCGAACATCGGAGGACCCCACTACCTTCTCCCGCC 300  
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QY 361 GSGCTCGGCTGGATGTCGCGATGCTGGGTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 420  
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QY 601 GCCCGCTTTTCTTCTTACCTTCTTACCTTCTTACCTTCTTACCTTCTTACCTTCTTACCTTCT 660  
Db 601 GCCCGCTTTTCTTCTTACCTTCTTACCTTCTTACCTTCTTACCTTCTTACCTTCTTACCTTCT 660  
QY 661 TAAAAATACATAATATGCTTTTTTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 720  
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Db 721 AAGGAG 780  
QY 781 GAAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
Db 781 GAAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
QY 841 TTTAAAAATGTCAA 853  
Db 841 TTTAAAAATGTCAA 853

RESULT 3  
US-08-581-918A-5  
; Sequence 5, Application US/08591918A  
; Patent No. 6043030  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Elliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPad  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/581,918A  
; FILING DATE: 02-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/497,214  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/346,147  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-071.06  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 853 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 213..587  
; US-08-581-918A-5

Query Match 100.0%; Score 853; DB 5; Length 853;  
Best Local Similarity 100.0%; Pred. No. 2.le-239;  
Matches 853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAGTACAGCAGCGGAGCATGGTGCAGGTTCTTGGTCACTGTAAAGATTTCAGCGCGC 60  
Db 1 GGAGTACAGCAGCGGAGCATGGTGCAGGTTCTTGGTCACTGTAAAGATTTCAGCGCGC 60  
QY 61 GGGCGCCCGCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAG 120  
Db 61 GGGCGCCCGCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAG 120  
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Db 181 AAGAGGGCGCACCGGAATCCTGGACACAGTGTATGATGGCAACGTTACGTAGCAG 240  
QY 241 CTCCTTCTGCTCAACTACGGTGCAGATTCGAACTCGGAGGACCCCACTACCTTCTCCCGCC 300  
Db 241 CTCCTTCTGCTCAACTACGGTGCAGATTCGAACTCGGAGGACCCCACTACCTTCTCCCGCC 300  
QY 301 CGGTGCACACGACGCGCGGGAAGGCTTCTTGACACGCTGTGTGCTGACGAGGCTCAG 360  
Db 301 CGGTGCACACGACGCGCGGGAAGGCTTCTTGACACGCTGTGTGCTGACGAGGCTCAG 360  
QY 361 GGGCTCGGCTGGATGTCGCGATGCTGGGTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 420



Patent No. 5723313  
GENERAL INFORMATION:  
APPLICANT: Sherr, Charles, J.  
APPLICANT: Quelle, Dawn, E.  
TITLE OF INVENTION: ARF-p19, A No. 5723313el Regulator of the Mammalian Cell  
TITLE OF INVENTION: Cycle  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 28-SEP-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Fox, Samuel, L.  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0656.0590000  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 713 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..548  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..551  
US-08-534-975-1

Query Match 78.9%; Score 672.8; DB 2; Length 713;  
Best Local Similarity 99.6%; Pred. No. 6.2e-187;  
Matches 685; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	1	GGAGTACAGCAGCGGAGCATGGGTGCGCAGGTTCTTGGTCACTGTAAAGGATTCAGCGCGC	60
DB	24	GGAGTACAGCAGCGGAGCATGGGTGCGCAGGTTCTTGGTCACTGTAAAGGATTCAGCGCGC	83
QY	61	GGCGCCGCGCTCCAGAGAGGGTTTCTTGGTGAAGTCTGTCGGATCCGCGAGACCCAG	120
DB	84	GGCGCCGCGCTCCAGAGAGGGTTTCTTGGTGAAGTCTGTCGGATCCGCGAGACCCAG	143
QY	121	GACAGGAGCTGCGCTCTGCTTTCGTGAACATGTTTTCAGGCTAGAGAGGATCTTGAG	180
DB	144	GACAGGAGCTGCGCTCTGCTTTCGTGAACATGTTTTCAGGCTAGAGAGGATCTTGAG	203
QY	181	AAGAGGCGCCACCGGAATCCTTGACACAGTGATGATGGCAACGTTTCAGCTAGCAG	240
DB	204	AAGAGGCGCCACCGGAATCCTTGACACAGTGATGATGGCAACGTTTCAGCTAGCAG	263
QY	241	CTCTTCTGCTCACTAGGTCGAGATTCGAACTCCGAGGACCCCACTACCTTCTCCGCC	300
DB	264	CTCTTCTGCTCACTAGGTCGAGATTCGAACTCCGAGGACCCCACTACCTTCTCCGCC	323
QY	301	CGGTGACGACGCGCGGAGGCTTCTGGACACGCTGGTGGTCTGCTGACGGGTGAG	360
DB	324	CGGTGACGACGCGCGGAGGCTTCTGGACACGCTGGTGGTCTGCTGACGGGTGAG	383

QY	361	GGGCTCGGCTGGATGTGCCGATGCTGGGTGCGCTGCGCTCGACTTGGCCCAAGAGC	420
DB	384	GGGCTCGGCTGGATGTGCCGATGCTGGGTGCGCTGCGCTCGACTTGGCCCAAGAGC	443
QY	421	GGGGACATCAAGACATCGTGCATATTTCCGTTCCGCTGGTGGTCTTGTGTTCCGCTG	480
DB	444	GGGGACATCAAGACATCGTGCATATTTCCGTTCCGCTGGTGGTCTTGTGTTCCGCTG	503
QY	481	GGTGTCTTTGTGTACCGTGGGAACGTCGCCACAGACCCGCGGCATAGCTTCAGCTCAA	540
DB	504	GGTGTCTTTGTGTACCGTGGGAACGTCGCCACAGACCCGCGGCATAGCTTCAGCTCAA	563
QY	541	GCACGCCAGGCGCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCC-CCCTC	599
DB	564	GCACGCCAGGCGCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCCGCGCTC	623
QY	600	AGCCGCGCTTTCTTCTTAGCTTCACTTCTAGCGATGCTAGCGTCTAGCGTGGCT	659
DB	624	AGCCGCGCTTTCTTCTTAGCTTCACTTCTAGCGATGCTAGCGTGGCT	683
QY	660	TTAAAAAATACATAATAATGCTTTTTT 687	
DB	684	TTAAAAAATACATAATAATGCTTTTTT 711	

RESULT 6  
US-08-954-470-1  
Sequence 1, Application US/08954470  
Patent No. 5876965  
GENERAL INFORMATION:  
APPLICANT: Sherr, Charles, J.  
APPLICANT: Quelle, Dawn, E.  
TITLE OF INVENTION: ARF-p19, A No. 5876965el Regulator of the  
TITLE OF INVENTION: Mammalian Cell Cycle  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 28-SEP-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: 08/534,975  
FILING DATE: 28-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fox, Samuel, L.  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0656.0590000  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 713 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..548

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; NAME/KEY: CDS
; LOCATION: 43..551
US-08-954-470-1

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Query Match	78.9%	Score	672.8	DB	3	Length	713		
Best Local Similarity	99.6%	Pred. No.	6.2e-187						
Matches	685	Conservative	0	Mismatches	2	Indels	1	Gaps	1
Qy	1	GGAGTACAGCAGCGGAGCATGGTGCAGAGTCTTGGTCACTGTAGGATTACAGCGCG	60						
Db	24	GGAGTACAGCAGCGGAGCATGGTGCAGAGTCTTGGTCACTGTAGGATTACAGCGCG	83						
Qy	61	GGCCGCCCACTCCAAAGAGAGAGGGTTTCTTGGTGAAGTTGTCGATCCCGGAGACCCAG	120						
Db	84	GGCCGCCCACTCCAAAGAGAGAGGGTTTCTTGGTGAAGTTGTCGATCCCGGAGACCCAG	143						
Qy	121	GACAGCGAGCTGCGCTCTGGCTTTTCGTGAACATGTTTGTGAGGCTAGAGGAGATCTTGAG	180						
Db	144	GACAGCGAGCTGCGCTCTGGCTTTTCGTGAACATGTTTGTGAGGCTAGAGGAGATCTTGAG	203						
Qy	181	AACAGGGCGCACCGGATCCTGGACAGGTGATGATGGCCACAGTTCACGTAGCAG	240						
Db	204	AACAGGGCGCACCGGATCCTGGACAGGTGATGATGGCCACAGTTCACGTAGCAG	263						
Qy	241	CTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACTCTTCGCCGCC	300						
Db	264	CTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACTCTTCGCCGCC	323						
Qy	301	CGGTGCAGCAGCAGCGGGGAAGGCTTCCTGGACAGCTGTGGTGTCTGCACGGGTGAC	360						
Db	324	CGGTGCAGCAGCAGCGGGGAAGGCTTCCTGGACAGCTGTGGTGTCTGCACGGGTGAC	383						
Qy	361	GGCTCGGCTGGATGTGGCGATGCTGGGGTGCCTGCGCTGCGCTTGGCCCAAGAGC	420						
Db	384	GGCTCGGCTGGATGTGGCGATGCTGGGGTGCCTGCGCTGCGCTTGGCCCAAGAGC	443						
Qy	421	GGGACATCAAGACATCGTGCATATTTGCTTCGGTGGGTGCTCTTTGTGTTCGGCTG	480						
Db	444	GGGACATCAAGACATCGTGCATATTTGCTTCGGTGGGTGCTCTTTGTGTTCGGCTG	503						
Qy	481	GGTGTCTTTGTGTACCGTGGGAACGTGCCACAGACCGACGGGCATAGCTTCAGGCTCAA	540						
Db	504	GGTGTCTTTGTGTACCGTGGGAACGTGCCACAGACCGACGGGCATAGCTTCAGGCTCAA	563						
Qy	541	GCACGCCAGGCCCTGGAACCTTCGCGCCAATCCCAGACGACAGCTAAATCC-GCCTC	599						
Db	564	GCACGCCAGGCCCTTGAACCTTCGCGCCAATCCCAGACGACAGCTAAATCCGCGCTC	623						
Qy	600	AGCCCGCCTTTTCTTCTTAGCTTCACCTTCTAGCGATGCTAGGCTGTCTAGCATGTGGCT	659						
Db	624	AGCCCGCCTTTTCTTCTTAGCTTCACCTTCTAGCGATGCTAGGCTGTCTAGCATGTGGCT	683						
Qy	660	TTAAAAATACATAATAATGCTTTTTT	687						
Db	684	TTAAAAATACATAATAATGCTTTTTT	711						

RESULT 7  
US-09-129-855A-1  
; Sequence 1, Application US/09129855A  
; Patent No. 6046032  
; GENERAL INFORMATION:  
; APPLICANT: Sherri, Charles, J.  
; APPLICANT: Quelle, Dawn, E.  
; TITLE OF INVENTION: ARF-p19, A No. 6046032el Regulator of the Mammalian  
; TITLE OF INVENTION: Cell Cycle  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue Suite 600  
; CITY: Washington  
; STATE: D.C.



APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 507 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 126..127 /note= "splice site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 467..468  
OTHER INFORMATION: /note= "Splice site"  
US-08-508-735-44

Query Match 44.8%; Score 382.2; DB 3; Length 507;  
Best Local Similarity 98.0%; Pred. No. 2.6e-102;  
Matches 387; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 196 GAATCTGCACAGGTGATGATGGGCAAGTTCAGGTAGCAGCTCTTGTCTCACT 255  
DB 113 GTACCCCGATTTCAGGTGATGATGGGCAAGTTCAGGTAGCAGCTCTTGTCTCACT 172  
QY 256 ACGGTGCAGATTCGAACTCGAGAGCCCACTACCTTCTCCGCCGCTGCACGACGACG 315  
DB 173 ACGGTGCAGATTCGAACTCGAGAGCCCACTACCTTCTCCGCCGCTGCACGACGACG 232  
QY 316 CGCGGAAGCTTCTGGACACGCTGGTGGTCTGCACGAGGTGAGGGCTCGGTGGATG 375  
DB 233 CGCGGAAGCTTCTGGACACGCTGGTGGTCTGCACGAGGTGAGGGCTCGGTGGATG 292  
QY 376 TCGCGATGCTGGGTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435  
DB 293 TCGCGATGCTGGGTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352  
QY 436 TCGTGCATATTTGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495  
DB 353 TCGTGCATATTTGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 412  
QY 496 CGCTGGGAAGCTGCGCCAGCAGCGGATGATGATGATGATGATGATGATGATGATGATG 555  
DB 413 CGCTGGGAAGCTGCGCCAGCAGCGGATGATGATGATGATGATGATGATGATGATGATG 472  
QY 556 TGAAGCTTCGCGCAATCCCAAGAGCAGAGCTAA 590  
DB 473 TGAAGCTTCGCGCAATCCCAAGAGCAGAGCTAA 507

RESULT 10  
US-08-474-177-25  
Sequence 25, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERM LINE MUTATIONS IN THE MTS GENE

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 395 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-474-177-25

Query Match 44.0%; Score 375; DB 1; Length 395;  
Best Local Similarity 98.5%; Pred. No. 2.9e-100;  
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGAGAGCCAGGACGCG-AGCTGC 133  
DB 1 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGAGAGCCAGGACGCGTCTGC 60  
QY 134 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGATCTTGAGAGAGGGCGGCAC 193  
DB 61 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGATCTTGAGAGAGGGCGGCAC 120  
QY 194 CGGAATCTCGGACCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 253  
DB 121 CGGAATCTCGGACCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
QY 254 CTACGGTGCAGATTCGAACCTCGGAGGACCCCACTACTCTCTCCCGCGGTGCAGACGC 313  
DB 181 CTACGGTGCAGATTCGAACCTCGGAGGACCCCACTACTCTCTCCCGCGGTGCAGACGC 240



Qy	314	AGCGCGGGAAGGCTTCCTTGACACGCTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA	373
Db	241	AGCGCGGAAGGCTTCCTTGACACGCTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA	300
Qy	374	TGTGCGGATGCCTGGGGTGCCTCGCGCTGCAGCTTGGCCCAAGACGGGGGACATCAAGA	433
Db	301	TGTCGCGATGCCTGGGGTGCCTCCCGCTGCAGCTTCGCCCAAGACGGGGGACATCAAGA	360
Qy	434	CATCGTCGATATTGGGTTCCGCTGGGTGCTCTT	468
Db	361	CATCGTCGATATTGGGTTCCGCTGGGTGCTCTT	395

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RESULT 11
US-08-487-033-25
; Sequence 25, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

```

Query Match	44.0%;	Score	375;	DR	2;	Length	395;
Best Local Similarity	98.5%;	Pred.	No. 2.9e-100;				
Matches	389;	Conservative	0;	Mismatches	5;	Indels	1;
Gaps							
QY	75	AAGAGAGGGTTTTCTTGTTGGAAGTTCTGTCGATCCCGGAGAPCCAGGACAGCG-AGCTGC	133				
DB	1	AAGAGAGGGTTTTCTTGTTGTAAGTTCTGTCGGATCCCGAGACCCAGACAGCTAGCTGC	60				
QY	134	GCCTCTGGCTTTCTGTAACATGTTTGTGAGGCTAGAGAGGATCTTGAGAGAGGGCGGCAC	193				
DB	61	GCCTCTGGCTTTCTGTAACATGTTTGTGAGGCTAGAGAGGATCTTGAGAGAGGGCGGCAC	120				
QY	194	CGAAATCTCGACAGGTGATGATGATGGGCAACGTTTCAGTAGCAGCTCTTCTGCTCAA	253				
DB	121	CGAAATCTCGACAGGTGATGATGATGGGCAACGTTTCAGTAGCAGCTCTTCTGCTCAA	180				
QY	254	CTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCGCGCCGCTGCACGACGC	313				
DB	181	CTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCGCGCCGCTGCACGACGC	240				
QY	314	AGCGCGGAAGGCTTCTTGACACGCTGGTGTGCTGCACGGGTCAAGGGCTCGGGCTGGA	373				
DB	241	AGCGCGGAAGGCTTCTTGACACGCTGGTGTGCTGCACGGGTCAAGGGCTCGGGCTGGA	300				
QY	374	TGTGCGGATGCTCGGGTGCCTCGCTCGCTGCAGCTTGGGCCAAGAGCGGGGACATCAAGA	433				
DB	301	TGTGCGGATGCTCGGGTGCCTCGCTCGCTGCAGCTTGGGCCAAGAGCGGGGACATCAAGA	360				
QY	434	CATCGTGCAGATTTGCGTTCCTCGGTGCTCTT	468				
DB	361	CATCGTGCAGATTTGCGTTCCTCGGTGCTCTT	395				
RESULT 12							
US-08-480-810-25							
; Sequence 25, Application US/08480810							
; Patent No. 5801236							
; GENERAL INFORMATION:							
; APPLICANT: Kamb, Alexander							
; TITLE OF INVENTION: MTS1 GENE							
; NUMBER OF SEQUENCES: 36							
; CORRESPONDENCE ADDRESS:							
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP							
; STREET: 1201 New York Avenue, Suite 1000							
; CITY: Washington							
; STATE: DC							
; COUNTRY: USA							
; ZIP: 20005							
; COMPUTER READABLE FORM:							
; MEDIUM TYPE: Floppy disk							
; COMPUTER: IBM PC compatible							
; OPERATING SYSTEM: PC-DOS/MS-DOS							
; SOFTWARE: PatentIn Release #1.0, Version #1.30							
; CURRENT APPLICATION DATA:							
; APPLICATION NUMBER: US/08/480,810							
; FILING DATE: 07-JUN-1995							
; CLASSIFICATION: 435							
; PRIORITY APPLICATION DATA:							
; APPLICATION NUMBER: PCT/US95/03316							
; FILING DATE: 17-MAR-1995							
; PRIOR APPLICATION DATA:							
; APPLICATION NUMBER: US 08/251,938							
; FILING DATE: 01-JUN-1994							
; PRIOR APPLICATION DATA:							
; APPLICATION NUMBER: US 08/215,087							
; FILING DATE: 18-MAR-1994							
; PRIOR APPLICATION DATA:							
; APPLICATION NUMBER: US 08/215,086							
; FILING DATE: 18-MAR-1994							
; PRIOR APPLICATION DATA:							
; APPLICATION NUMBER: US 08/227,369							



APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 395 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-848-251-25

Query Match 44.08; Score 375; DB 4; Length 395;  
Best Local Similarity 98.59; Pred. No. 2.9e-100;  
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 75 AAGAGAGGTTTCTTGTGTAAGTTCTGGCGATCCCGAGACCCAGGACCG-AGCTGC 133  
|||||  
Db 1 AAGAGAGGTTTCTTGTGTAAGTTCTGGCGATCCCGAGACCCAGGACCGTAGCTGC 60  
Qy 134 GCTCTGGCTTTCGTAACATCTTGTGAGGCTAGAGGATCTTGAGAAGAGGCCCGCAC 193  
|||||  
Db 61 GCTCTGGCTTTCGTAACATCTTGTGAGGCTAGAGGATCTTGAGAAGAGGCCCGCAC 120

Qy 194 CGGAATCCTGGACACAGGTGATGATGGGCAACGTTACGTACGAGCTCTTGTCTCAA 253  
|||||  
Db 121 CGGAATCCTGGACACAGGTGATGATGGGCAACGTTACGTACGAGCTCTTGTCTCAA 180  
Qy 254 CTACGGTGCAGATTCGAACATGCGAGGACCCCACTACTCTTCCCGCCGGTGCACGACGC 313  
|||||  
Db 181 CTACGGTGCAGATTCGAACATGCGAGGACCCCACTACTCTTCCCGCCGGTGCACGACGC 240  
Qy 314 AGCGCGGAAGGCTTCTCTGACACAGCGTGGTGTGCTGCACGCGGTACGGGCTCGGCTGA 373  
|||||  
Db 241 AGCGCGGAAGGCTTCTCTGACACAGCGTGGTGTGCTGCACGCGGTACGGGCTCGGCTGA 300  
Qy 374 TGTGCGGATGCGCTGGGTCGCTCGGCTCGACTTGGCCCAAGAGCGGGACATCAAGA 433  
|||||  
Db 301 TGTGCGGATGCGCTGGGTCGCTCGGCTCGACTTGGCCCAAGAGCGGGACATCAAGA 360  
Qy 434 CATCGTGCATATTTCGTTCCGCTGGGTGCTCTT 468  
|||||  
Db 361 CATCGTGCATATTTCGTTCCGCTGGGTGCTCTT 395

## RESULT 15

US-08-486-047-25  
; Sequence 25, Application US/08486047  
; Patent No. 5994095  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS2 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,047  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 395 base pairs

;  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-486-047-25

Query Match 44.0%; Score 375; DB 4; Length 395;  
Best Local Similarity 98.5%; Pred. No. 2.9e-100;  
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
  
QY 75 AAGAGAGGTTTTCTTGGTGAAGTTCTGCGATCCCGAGACCCAGGACGCG-AGCTGC 133  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 1 AAGAGAGGTTTTCTTGGTGAAGTTCTGCGATCCCGAGACCCAGGACGCGTAGCTGC 60  
  
QY 134 GCTCTGGCTTTCTGTAACATGTTGTAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 193  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 GCTCTGGCTTTCTGTAACATGTTGTAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 120  
  
QY 194 CGGAATCCTTGGACCGAGTGATGATGGCAACGTTTACGTAGCAGCTCTTCTGCTCAA 253  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 CGGAATCCTTGGACCGAGTGATGATGGCAACGTTTACGTAGCAGCTCTTCTGCTCAA 180  
  
QY 254 CTACGGTGCAGATTGCACTGCGAGAGCCCACTACCTTCTCCCGCCCGGTGCAGAGGC 313  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 181 CTACGGTGCAGATTGCACTGCGAGAGCCCACTACCTTCTCCCGCCCGGTGCAGAGGC 240  
  
QY 314 AGCGCGGAAGGCTTCCCTGGACACGCTGGTGTGCTGCACGGGTGAGGGGCTCGGCTGGA 373  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 241 AGCGCGGAAGGCTTCCCTGGACACGCTGGTGTGCTGCACGGGTGAGGGGCTCGGCTGGA 300  
  
QY 374 TGTGGCGGATGCTGGGGTTCGCTCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGA 433  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 301 TGTGGCGGATGCTGGGGTTCGCTCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGA 360  
  
QY 434 CATCGTGCAGATTGCGGTTCGCGTGGGTGCTCTT 468  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 361 CATCGTGCAGATTGCGGTTCGCGTGGGTGCTCTT 395

Search completed: July 21, 2000, 06:06:41  
Job time: 13807 sec

Gencore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 02:48:45 ; Search time 1049.06 Seconds  
(without alignments)  
3585.670 Million cell updates/sec

Title: US-09-016-869A-5  
Perfect score: 853  
Sequence: 1 GGAGTACAGCAGCGGACCA.....GATACTTTTAAATGTCAA 853

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues 10495684  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

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2:	em_est2:*
3:	em_est3:*
4:	em_est4:*
5:	em_est5:*
6:	em_est6:*
7:	em_est7:*
8:	em_est8:*
9:	em_est9:*
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11:	em_est11:*
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111:	em_gss10:*
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114:	gb_gss11:*
115:	em_gss12:*
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Db 488 GCCTGCGGACCCGACCTCTCACCCGACCCCTGCACGACGCTGCCGGGAGGGCTTCCTGG 429
QY 334 ACACGCTGGTGGTCTGCACGGGTCAAGGGCTCGGCTGGATGTCGGGATGCTTGGGGTC 393
Db 428 ACACGCTGGTGGTCTGCACCGGCGCGGGCTGGACGTCCGCGATGCTTGGGGCC 369
QY 394 GCCTGCGGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTCCGATATTTCGGTT 453
Db 368 GTCTGCCGCTGGACCTGGCTGAGAGCTGGGGCCATCGCATGTCGCACGCTACTCTGGCG 309
QY 454 CGCTGGGGTG 463
Db 308 CGCTGCGGG 299

RESULT 2
AI363262/c
LOCUS
DEFINITION
qy56f03.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3'
similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ; contains
LTR9.b3 TAR1 repetitive element ; , mRNA sequence.
ACCESSION
AI363262
VERSION
AI363262.1 GI:4114883
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 708)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BrGAP), Tumor Gene Index
Unpublished (1998)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 872 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2016029"
/clone_lib="NCI-CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGGAGCGCGCGGATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 137 a 210 c 219 g 140 t 2 others
ORIGIN

Query Match 21.3%; Score 181.6; DB 38; Length 708;
Best Local Similarity 67.1%; Pred. No. 1e-39;
Matches 286; Conservative 0; Mismatches 136; Indels 4; Gaps 2;

```

```

QY 41 ACTGTAAGATTACAGCGCGGGCCGCCCTACTCCAGAGAGGGTTTCTTGGTGAAGTTC 100
Db 708 ACCCTCGGAATTCGGCGCGCGTTCGGCCCGCGAGTAGGGG-TTTCGTGGTTCATC 650
QY 101 GTCGGATCCGGAGACCCAGGACAGCGAGTGGCTTCGCTTTCGTGAACATGTTGTTG 160
Db 649 CACAGTCACTACNGGGAGTGGGCGAGCGCAAGGGGCGCCGCCCTGTGGCTTCGTGCTG 590
QY 161 AGCTAGAGAGATCTTTGAGAAGAGGGGCGCACCCGGAATCTCTG---GACCAAGTGTATG 217
Db 589 ATGCTACTAGAAAGCCAGCGTCTAGGCGAGCAGCCGCTTCTCTAGAGANCAGGTCTATG 530
QY 218 GATGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGCTGCAGATTCGAACCTGCGA 277
Db 529 GATGGCAAGCGCCGAGTGGCGAAGCTGTGCTGCCGGGCGCGAGGCCCAACTGCGA 470
QY 278 GGACCCCACTACCTTCTCCCGCGCTGCACGACGACGCGGGAAGGCTTCTCTGGACAC 337
Db 469 CGACCCGCAACTCTCACCCGACCCCTGCACGACGCTGCCGGGAGGGCTTCTCTGGACAC 410
QY 338 GCTGGTGGTGTGTCACGGGTCAAGGGCTCGGCTGGATGTGCGGATGCTTGGGGTGGCCT 397
Db 409 GCTGGTGGTGTGTCACCGGGCGCGGCTGGAGCTGCGGATGCTTGGGGGCGCTCT 350
QY 398 GCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGGGATATTTCGTTCCGC 457
Db 349 GCGCTGGACTGCTGAGAGCTGGGCCATCGCGATGTGCGACGCTACCTGCGCGCGC 290
QY 458 TGGGTG 463
Db 289 TGGGG 284

RESULT 3
AI328496
LOCUS
DEFINITION
ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
sequence.
ACCESSION
AI328496
VERSION
AI328496.1 GI:6798992
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 648)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
On Apr 7, 1998 this sequence version replaced gi:3036295.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Edge BioSystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLC0030 row: 0 column: 24
Seq primer: -21M13 forward primer (AB1).
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2847599"
/clone_lib="NIH_MGC_4"
/cell_line="MGCl"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Cervix; Vector: pOTB7a; Site_1: ScaI;
Site_2: CeuI; cDNA made by oligo-dT priming.

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Directionally cloned into Ceul/SceI sites using the following 5' adaptor: taactaacgtcttaagtagcga and 3' adaptor: ttctattacctcttctcgaccacataaa. Average insert size 900 bp. Library prepared by Edge Biosystems.

```
BASE COUNT      127 a   200 c   196 g   123 t     2 others
ORIGIN

Query Match      20.6%; Score 175.8; DB 71; Length 648;
Best Local Similarity 71.2%; Pred. No. 4.1e-38;
Matches 247; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

Qy 120 GGACAGGAGTGGCGCTCTGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGA 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19 GGGCAGCCAGGGGCGCCCGCTGTCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 78

Qy 180 GAAGAGGCGCCGACCGGAATCT---GGACCAGGTGATGATGGCGACGTTACGTA 236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 GTCTAGGCGCAGCAGCGCTTCTTAGAAGACCAGGTCTATGATGGCGAGCGCCGAGTG 138

Qy 237 GCAGCTCTCTCTCAACTACGGTGCAGATTCGAATCCGAGGACCCCACTACCTTCTCC 296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 GCGAGCTGCTGCTCTCCAGCGCGGAGCCCACTGCGCGACCCGCGCACTCTCACC 198

Qy 297 GCGCGGTGCAGAGCAGCGCGGAGAGCTTCTTGACAGCTGTGTGTGCTGCACGGG 356
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 GCACCGTGCAGAGCTGCTGCGCGGAGGCTTCTTGGACACGCTGTGTGTGCTGCACCG 258

Qy 357 TCAGGGCTCGGCTGGATGCGCGATGCGCGGTCGCGGTCGCGCTGCGCTGCGCTGCG 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 GCGCGGGCGGCTGGAGCTGCGGATGCTTGGGCGCTGTCGCGCTGCGCTGCGCTGCG 318

Qy 417 GAGCGGGACATCAAGACATCGTGCATATTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 463
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 GAGCTGGCCATCGGATGTCGACGTACTGCGCGCGGCTGCGGG 365

RESULT 4
AI765096/c      774 bp      mRNA      EST      21-DEC-1999
LOCUS      w148b08.x1 NCI.CGAP.Col6 Homo sapiens cDNA clone IMAGE:2393463 3'
DEFINITION      similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
                  LTR9.83 MER22 repetitive element ;, mRNA sequence.
ACCESSION      AI765096
VERSION      AI765096.1 GI:5231605
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 774)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      On Feb 22, 1999 this sequence version replaced gi:4283180.
               Contact: Robert Strausberg, Ph.D.
               Tel: (301) 496-1550
               Email: Robert_Strausberg@nih.gov
               Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
               M.D., Ph.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Insert Length: 854 Std Error: 0.00
               Seq primer: -400P from Gibco
               High quality sequence stop: 400.
               Location/Qualifiers
               1. 774
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/db_xref="taxon:9606"
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/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/Note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI.CGAP.Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaudo. "

BASE COUNT      153 a   220 c   221 g   179 t     1 others
ORIGIN

Query Match      19.4%; Score 165.6; DB 44; Length 774;
Best Local Similarity 66.9%; Pred. No. 2.8e-35;
Matches 295; Conservative 0; Mismatches 140; Indels 6; Gaps 4;

Qy 29 AGGTTCTTGCTCACTTAAGGATTCAGCGCGCGCGCCCACTCCAGAGAGGGTTTC 88
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 774 AGGTTCTTGCTCACTTAAGGATTCAGCGCGCGCGCCCACTCCAGAGAGGGTTTC 715

Qy 89 TTGG-TGAAGTTGTCGATCCCGGAGACCCAGACAGCAGCTGCGC-TCTGGCTTTCG 146
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 714 GTGGTTACATCCCGGGCTCACGGGGAGGTGGCAGCGCCAGGGCGGCCCGCTGT 655

Qy 147 TGAACATGTTGTAGGCTAGAGAGGA-TCTTTGAGAAGAGGGCCGACCGAATCCT--- 202
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 654 GGGCCATCGTCTTATGCTATTAGGAGAGCCAGCGCTTTAGGAGCAGCAGCGCTTCTCTAGA 595

Qy 203 GGACAGGTGATGATGGGCAACGTTTCAGTACAGCTCTTCTGCTCACTACGGTGC 262
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Db 594 AGACAGGTGATGATGGGCAACGTTTCAGTACAGCTCTTCTGCTCACTACGGTGC 535

Qy 263 AGATTGCAACTCGAGGACCCCACTACCTTCTCCGCGCGGTGACAGCAGCGCGGGA 322
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Db 534 GGAGCCCAATTGGCGCGACCCCGCCACATTTACCCGACCGCTGACAGCGCTGCCCGGGA 475

Qy 323 AGGCTTCTTGACAGCTGGTGGTGTGCTGACGGGTGAGGGGCTCGGCTGGATGCGGGA 382
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Db 474 GGGCTTCTTGACAGCTGGTGGTGTGCTGACCGGGCGCGCGCTGCGCTGCGCAA 415

Qy 383 TGCGTGGGTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
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Db 414 TGCGTGGGTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355

Qy 443 ATATTGCGCTTCCGCTGGGTG 463
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Db 354 GTACCTGCGCGCGCTTCGGG 334

RESULT 5
AI765096/c      590 bp      mRNA      EST      07-MAR-2000
LOCUS      w181d11.x1 NCI.CGAP.Br25 Homo sapiens cDNA clone IMAGE:2431317 3'
DEFINITION      similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
                  ;, mRNA sequence.
ACCESSION      AI765096
VERSION      AI765096.1 GI:5545430
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 590)
AUTHORS      NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute / National Institute of Neurological
               Disorders and Stroke, Brain Tumor Genome Anatomy Project
```



**JOURNAL**  
**COMMENT**  
(CGAP/BTGP), Tumor Gene Index  
Unpublished (1998)  
On Oct 30, 1998 this sequence version replaced gi:3813427.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 845 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 444.

**FEATURES**  
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/clone="IMAGE:2431317"  
/clone\_lib="NCI\_CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 114 a 158 c 179 g 139 t  
ORIGIN

Query Match 18.8%; Score 160.2; DB 45; Length 590;  
Best Local Similarity 73.6%; Pred. No. 8.1e-34;  
Matches 204; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
QY 187 GCCGACCGGAATCTCGACCAAGTGTATGATGGGCGACGTTACGTACGACTCTTC 246  
DB 586 GCAGCCGCTTCATAGAACACAGCTCATGATGGGCGACGCGCAGAGTGGCGGAGCTGC 527  
QY 247 TGCTCAACTAGCGTGCAGATTTCGAACATGCGAGGACCCACTACCTTCTCCGCCCGCTGC 306  
DB 526 TGCTGCTCCAGCGCGGAGCCCAACTTGGCGGACCCCGCCACTCTCACCGACCCGCTGC 467  
QY 307 ACGACGACGCGCGGAGAGGCTTCTCGACACGCTGGTGGTGTCTGCTACGCGGTTCAGGGGCTC 366  
DB 466 ACGACGCTGCCGCGGAGGGCTTCTCGACACGCTGGTGGTGTCTGCTACGCGGCGCGGCGC 407  
QY 367 GGCTGGATGTGCGCGATGCTTGGGGTGCCTGCGCTGCGACTTGGCCCAAGAGCGGGGAC 426  
DB 406 GGCTGGAGCTGCGCGATGCTTGGGGGCGCTGCGCGGTGGACCTGCTGAGGAGCTGGGCC 347  
QY 427 ATCAAGACATCGTCCGATATTTGGTTCCTCGCTGGGTG 463  
DB 346 ATCCGATGTCCACAGTACCTGCGCGGCGTGGCGG 310

**RESULT 6**  
AI870879/c  
**LOCUS** AI870879 579 bp mRNA EST 07-MAR-2000  
**DEFINITION** w177d11.x1 NCI\_CGAP\_Brn25 Homo sapiens CDNA clone IMAGE:2430933 3'  
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
; mRNA sequence.  
**ACCESSION** AI870879  
**VERSION** AI870879.1 GI:5544847  
**KEYWORDS** EST.

**SOURCE**  
**ORGANISM** human.  
**REFERENCE** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 579)  
**AUTHORS** NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**TITLE** National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGP), Tumor Gene Index  
**JOURNAL** Unpublished (1998)  
**COMMENT** On May 18, 1998 this sequence version replaced gi:3136859.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 819 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 474.

**FEATURES**  
source  
Location/Qualifiers  
1..579  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2430933"  
/clone\_lib="NCI\_CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 113 a 157 c 182 g 127 t  
ORIGIN

Query Match 18.5%; Score 157.6; DB 45; Length 579;  
Best Local Similarity 75.4%; Pred. No. 4.2e-33;  
Matches 196; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 204 GACCAGTGTATGATGGGCAACGTTACGTACGAGCTCTTCTGTCTCAACTACGTTGCA 263  
DB 558 GACCAGTGTATGATGGGCGAGTGGCGGAGTGTCTGCTGCTCCACGGCGCG 499  
QY 264 GATTCGACTGCGAGGACCCCACTACCTTCTCCGCCCGCTGCGACGCGCGGGAA 323  
DB 498 GAGCCCAACTGCGCGACCCCGCCCACTCTCACCGACCCCGTGCACGCGTGGCGGGAG 439  
QY 324 GGCTTCTCGACACGCTGGTGGTGTGCTGACGGGCTCGGCTGGATGTGCGCGAT 383  
DB 438 GGCTTCTCGACACGCTGGTGGTGTGCTGACCGGGCGCGGCTGGACGTGGCGGAT 379  
QY 384 GCCTGGGGTCCGCTGCGGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGC 443  
DB 378 GCCTGGGGCGCTGCTCCCGTGGACCTGGCTGAGGAGCTGGCCATCGCGATGTCGAC 319  
QY 444 TATTGGCTTCCGCTGGGTG 463  
DB 318 TACCTGCGCGGCTGCGGG 299  
**RESULT 7**







/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTCACATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaudo."

BASE COUNT 106 a 143 c 165 g 114 t  
ORIGIN

Query Match 16.5%; Score 140.4; DB 45; Length 528;

Best Local Similarity 75.7%; Pred. No. 2.4e-28; Matches 174; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 234 GTAGCAGCTCTTCTGCTCAACTACGCTGCAGATTGCAACTGCGAGGACCCCACTACTCTC 293

Db 528 GTGGCGGAGCTGCTGCTCCACGGCGGAGCCCACTGCGCCGACCCCGCACTCTC 469

QY 294 TCCGCGCCGCTGCACGACGCGCGGAGAGGCTTCTTGACACGCTGGTGGTGGCTGCAC 353

Db 468 ACCGACCCGCTGCACGACGCTGCCGAGGAGGCTTCTTGACACGCTGGTGGTGGCTGCAC 409

QY 354 GGTGACGGGCTCGGTGGATGTCGCGGATGCTGGGGTCCGCTGCGCTGCATGGGCG 413

Db 408 CGGGCGGGGCGGGCTGGACGTCGCGATGCTGGGGCGGCTGCGCCGTGGACCTGGCT 349

QY 414 CRAAGCGGGGACATCAAGACATCGTCGATATTTCGCTCCGCTGGGTG 463

Db 348 GAGGAGCTGGGCGCATCGGATGTCGACGCTACTCGGCGCGCTGCGGG 299

RESULT 13  
AI638416/c

LOCUS tt31903.x1 NCI\_CGAP\_G66 Homo sapiens cDNA clone IMAGE:2242420 3'  
DEFINITION similar to TR:O16361 O16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI638416  
VERSION AI638416.1 GI:4690650

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Apr 7, 1998 this sequence version replaced gi:3036438.

Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaudo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

Cloning Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 648 Std Error: 0.00

Seq primer: -400P from Gbco

High quality sequence stop: 462.

Location/Qualifiers

1..528

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/db\_xref="taxon:9606"

/clone="IMAGE:2242420"

FEATURES  
source

/clone\_lib="NCI\_CGAP\_G66"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI\_CGAP\_G64 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaudo."

BASE COUNT 106 a 143 c 163 g 114 t 2 others  
ORIGIN

Query Match 16.4%; Score 140; DB 42; Length 528;

Best Local Similarity 75.2%; Pred. No. 3e-28; Matches 173; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 234 GTAGCAGCTCTTCTGCTCAACTACGCTGCAGATTGCAACTGCGAGGACCCCACTACTCTC 293

Db 525 GTGGCGGAGCTGCTGCTCCACGGCGGAGCCCACTGCGNCGACNCCGCACTCTC 466

QY 294 TCCGCGCCGCTGCACGACGCGGGAAGGCTTCTTGACACGCTGGTGGTGGCTGCAC 353

Db 465 ACCGACCCGCTGCACGACGCTCCGCGGAGGCTTCTTGACACGCTGGTGGTGGCTGCAC 406

QY 354 GGTGACGGGCTCGGTGGATGTCGCGGATGCTGGGGTCCGCTCGGACTTGGGC 413

Db 405 CGGGCGGGGCGGCTGGACGCTGCGGATGCTGGGGCGGCTGCGCCGTGGACCTGGCT 346

QY 414 CRAAGCGGGGACATCAAGACATCGTCGATATTTCGCTCCGCTGGGTG 463

Db 345 GAGGAGCTGGGCGCATCGGATGTCGACGCTACTCGGCGGCGCTGCGGG 296

RESULT 14  
AI633790/c

LOCUS tt28e10.x1 NCI\_CGAP\_G66 Homo sapiens cDNA clone IMAGE:2242122 3'  
DEFINITION similar to TR:O16361 O16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM  
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI633790  
VERSION AI633790.1 GI:4685120

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 531)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index.

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaudo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

Cloning Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 623 Std Error: 0.00

Seq primer: -400P from Gbco

High quality sequence stop: 454.

Location/Qualifiers

1..531

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/clone="IMAGE:2242122"
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/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1459084-1470983, and 1475392-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      107 a 144 c 163 g 116 t      1 others
ORIGIN

Query Match      16.3%; Score 139.4; DB 42; Length 531;
Best Local Similarity 75.2%; Pred. No. 4.4e-28;
Matches 173; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 234 GTACGAGCTCTTCTCACTACGGTGCAGATTCGAACCTCGAGGACCCACTACCTTC 293
Db 528 GTGCGGAGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCGGACCCCACTTC 469
QY 294 TCCGCGCGGCTGACGACGACGCGGAGAGGCTTCCTGGACACAGCTGCTGCTGCAC 353
Db 468 ACCGACCCGTCGACGACGCTGCTGCGGAGGCTTCTTGACACGCTGCTGCTGCAC 409
QY 354 GGGTCAGGGCTCGGCTGGATGTCGGCGATGCTGGGGTGCCTGCGCTGCGCTGGGCC 413
Db 408 CGGGCGGGCGCGGCTGGAGTGCAGTGCCTGGGGCGGCTGCGCGTGGACCTGGCT 349
QY 414 CAAGAGCGGGGACATCAAGACATCGCGATATTTGCTTCGCTGGGTG 463
Db 348 GAGGAGCTGGGCCATCGCGATGTCGACAGTACCTGCGCGCGCTGCGGG 299

RESULT 15
AW631047
LOCUS      AW631047      480 bp      mRNA      EST      31-MAR-2000
DEFINITION hp91d11.y1 NCI_CGAP_GUI Homo sapiens cDNA clone IMAGE:2970165 5'
similar to SW:CDN2.HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A ; mRNA sequence.
ACCESSION  AW631047
VERSION     AW631047.1 GI:7377837
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 480)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     On Jan 6, 2000 this sequence version replaced gi:6676951.
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 314.
Location/Qualifiers
1. .480
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/clone="IMAGE:2970165"
/clone_lib="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: Sali; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."
BASE COUNT      94 a 144 c 135 g 107 t
ORIGIN

Query Match      15.6%; Score 133.4; DB 79; Length 480;
Best Local Similarity 74.9%; Pred. No. 2e-26;
Matches 167; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 207 CAGGTGATGATGATGGCAACGTTTACGTAGCAGCTTTCTCTCAACTACGGTGCAGAT 266
Db 256 CAGGTGATGATGATGGCAGCGCGCGTGGGAGCTGCTGCTCCACGCGCGGAG 315
QY 267 TCGAACTGGGAGGACCCCACTACCTTTCCCGCGCGGTGGAGCAGCAGCGCGGAGGC 326
Db 316 CCCAACTGGCAGACCCCTGCCACTCTCACCGCGCGGTGATGCTGCCCGGAGGC 375
QY 327 TTCCCTGGACAGCTGGTGTGCTGCACGGGTCCAGGGGCTCGGCTGGATGTCGCGATGCC 386
Db 376 TTCCCTGGACAGCTGGTGTGCTGTACCGTCCCGGGGCGCGCTTGACGTGCACCTATGCT 435
QY 387 TGGGTCGCCCTGCCCTCGACTTGGCCCCAAGAGCGGGGACATC 429
Db 436 CTGGGTCTGCTGCCCATAGACTTGTCCGAAGAACTGGGTGACC 478

Search completed: July 21, 2000, 02:48:50
Job time: 9645 sec
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\*\*\*\*\*  
WPSRELH  
\*\*\*\*\*  
(TM)

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MParch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:41:29 2000; MasPar time 6.47 Seconds  
Tabular output not generated. 457.636 Million cell updates/sec

Title: >US-09-016-869A-6  
Description: (1-125) from US09016869A.pep  
Perfect Score: 892  
Sequence: 1 MMGNVHVALLNYGADSN.....SFSSSTPRALELRGQSQEQS 125

Scoring table: PAM 150  
Gap 11

Searched: 189963 seqs, 23586106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a:geneseq36  
1:geneseq

Statistics: Mean 29.993; Variance 124.567; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	892	100.0	125	1	Murine INK4a-p16 C-ter	3.05e-77
2	892	100.0	125	1	Cell-cycle regulatory	3.05e-77
3	892	100.0	168	1	Mouse multiple tumour	3.05e-77
4	723	81.1	127	1	Cell-cycle regulatory	3.90e-60
5	473	53.0	105	1	A human multiple tumour	3.94e-35
6	473	53.0	105	1	Multiple tumour suppressor	3.94e-35
7	473	53.0	105	1	Amino acid sequence 1	3.94e-35
8	473	53.0	105	1	Human multiple tumour	3.94e-35
9	473	53.0	105	1	Human multiple tumour	3.94e-35
10	473	53.0	105	1	Human MTS1E1-beta prot	3.94e-35
11	473	53.0	148	1	Multiple tumour suppressor	3.94e-35
12	473	53.0	148	1	Human multiple tumour	3.94e-35
13	473	53.0	151	1	Inhibitor of cyclin de	3.94e-35
14	473	53.0	151	1	Amino acid sequence of	3.94e-35
15	473	53.0	156	1	Cell-cycle regulatory	3.94e-35
16	473	53.0	156	1	Tumour suppressor p16.	3.94e-35
17	473	53.0	156	1	A human multiple tumour	3.94e-35
18	473	53.0	156	1	Human multiple tumour	3.94e-35
19	473	53.0	156	1	Human MTS1 protein.	3.94e-35
20	473	53.0	237	1	Truncated p27/p16 fusi	3.94e-35
21	473	53.0	252	1	Truncated p27/p16 fusi	3.94e-35
22	473	53.0	334	1	Truncated p27/p16 fusi	3.94e-35
23	473	53.0	365	1	Human p16p27 fusion pr	3.94e-35

24	473	53.0	365	1	W95096	Human p16p27 fusion pr	3.94e-35
25	473	53.0	365	1	W23536	CDK inhibitory fusion	3.94e-35
26	473	53.0	380	1	W23535	CDK inhibitory fusion	3.94e-35
27	473	53.0	380	1	W95095	Human p16(GS)p27 fusio	3.94e-35
28	473	53.0	391	1	W95094	Human p27-p16 fusion p	3.94e-35
29	473	53.0	391	1	W23534	CDK inhibitory fusion	3.94e-35
30	472	52.9	138	1	W74553	Amino acid sequence 2	4.95e-35
31	472	52.9	138	1	W40526	Human MTS2 protein.	4.95e-35
32	472	52.9	138	1	R81702	Multiple tumour suppressor	4.95e-35
33	472	52.9	138	1	W19255	Human multiple tumour	4.95e-35
34	472	52.9	138	1	W80526	A human multiple tumour	4.95e-35
35	472	52.9	138	1	R80948	Human multiple tumour	4.95e-35
36	464	52.0	156	1	W19252	Human multiple tumour	3.05e-34
37	461	51.7	130	1	W70823	Mouse multiple tumour	6.04e-34
38	460	51.6	138	1	R85117	Cell-cycle regulatory	7.52e-34
39	459	51.5	130	1	R85118	Cell-cycle regulatory	9.52e-34
40	456	51.1	156	1	W19253	Human multiple tumour	1.88e-33
41	453	50.8	348	1	W95104	Truncated p27/p16 fusi	3.72e-33
42	439	49.2	85	1	R85113	Cell-cycle regulatory	8.93e-32
43	439	49.2	138	1	R85115	Cell-cycle regulatory	8.93e-32
44	439	49.2	157	1	R85114	Cell-cycle regulatory	8.93e-32
45	396	44.4	67	1	W16324	Human INK4a-p16 C-term	1.48e-27

ALIGNMENTS

RESULT 1  
ID W16322 standard; Protein; 125 AA.  
AC W16322;  
DT 16-AUG-1997 (first entry)  
DE Murine INK4a-p16 C-terminal fragment.  
KW INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6; retinoblastoma;  
KW cancer; tumour; ARF-p19; alternative reading frame; cell cycle;  
KW therapy; wound healing.  
OS Mus musculus.  
PN W09712060-A1.  
PD 03-APR-1997.  
PF 25-SEP-1996; U15312.  
PR 27-SEP-1995; US-534975.  
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
PI Quelle DE, Sherr CJ;  
DR WPI: 97-212919/19.  
DR N-PSDB; T62485.  
DR Nucleic acid encoding ARF-p19 which induces cell cycle arrest when  
PT overexpressed - used for diagnosis and treatment of cancer, and for  
PT drug screening  
PS Example 1; Fig 1; 49pp; English.  
CC A polypeptide (W16322) comprises the C-terminal region of murine  
CC INK4a-p16, a specific inhibitor of the cyclin D-dependent kinases  
CC CDK4 and CDK6. The partial polypeptide sequence is encoded by  
CC exon 2 (see also T62485) of the INK4A gene. An syntactically  
CC overlapping reading frame, also including exon 2, has been  
CC identified that codes for a novel protein, ARF-p19 (W16321),  
CC which induces cell cycle arrest when overexpressed. INK4a-p16  
CC can block CDK4 and CDK6 from phosphorylating the retinoblastoma  
CC protein (pRb), preventing exit from the G1 phase of the cell  
CC cycle. Deletions and mutations involved in the INK4A gene occur  
CC frequently in cancer cells, suggesting that INK4a-p16  
CC suppresses tumour formation.  
SQ Sequence 125 AA;

Query Match 100.0%; Score 892; DB 1; Length 125;  
Best Local Similarity 100.0%; Pred. No. 3.05e-77;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MMGNVHVALLNYGADSNCEPTTFSPVHDAAREGFLDTLVHLHSGARLDVRDAG	60
QY	1	MMGNVHVALLNYGADSNCEPTTFSPVHDAAREGFLDTLVHLHSGARLDVRDAG	60
Db	61	RLPLDLAQRGHQDHYVYLRSGACSCSAGWSLCTAGNAQTGDGHFSSSTPRALELRGQ	120
QY	61	RLPLDLAQRGHQDHYVYLRSGACSCSAGWSLCTAGNAQTGDGHFSSSTPRALELRGQ	120



Db 121 SOEQS 125  
QY 121 SOEQS 125

## RESULT 2

ID R85120 standard; Protein; 125 AA.  
AC R85120;  
DT 01-MAR-1996 (first entry)  
DE Cell-cycle regulatory protein p13.5.  
KW Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;  
KW CCR; cancer; cell proliferation.  
OS Mus sp.  
PN W09528483-A1.  
PD 26-OCT-1995.  
PR 14-APR-1995; U04636.  
PR 14-APR-1994; US-227371.  
PR 25-MAY-1994; US-248812.  
PR 14-SEP-1994; US-306511.  
PR 29-NOV-1994; US-346147.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;  
FI N-PSDB; T02965.  
DR New cell cycle regulating proteins bind to cyclin dependent kinase -  
PT and related nucleic acids, antibodies etc., used in diagnosis and  
PT therapy of abnormal cell proliferation, degeneration etc.  
PS Example 5; Page 81; 109pp; English.  
CC The mouse cell-cycle regulatory (CCR) protein p13.5 (R85120) was  
CC obtd. by expression of a cDNA clone (T02965) isolated from  
CC mouse embryonal stem cells. CCR p13.5 specifically inhibits the  
CC activity of cyclin-dependent kinases during various stages of the  
CC cell cycle, and can be used in the treatment and diagnosis of  
CC proliferative disorders.  
SQ Sequence 125 AA;

Query Match 100.0%; Score 892; DB 1; Length 125;  
Best Local Similarity 100.0%; Pred. No. 3.05e-77;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 60  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 60  
Db 61 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
QY 61 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
Db 121 SOEQS 125  
QY 121 SOEQS 125

## RESULT 3

ID W80527 standard; Protein; 168 AA.  
AC W80527;  
DT 03-FEB-1999 (first entry)  
DE Mouse multiple tumour suppressor 1 (MTS1) protein.  
KW Murine; multiple tumour suppressor 1 gene; MTS1; cancer.  
OS Mus musculus.  
PN US5843756-A.  
PD 01-DEC-1998.  
PR 28-JUL-1995; 058735.  
PR 28-JUL-1995; US-508735.  
PR 07-JUN-1995; US-487033.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Jiang P, Kamb A, Stone S;  
DR WPI; 99-044585/04.  
DR N-PSDB; V70623.  
PT Mouse multiple tumour suppressor gene segment - useful for primer  
PS design  
PS Example 7; Fig 19; 80pp; English.  
CC The present sequence represents mouse multiple tumour suppressor 1

CC (MTS1) gene. The MTS1 gene can be used to design primers to  
CC detect abnormalities i.e. polymorphisms which may predispose  
CC towards malignancies such as melanoma, leukaemia, astrocytoma,  
CC lymphoma, glioma, as well as tumours of e.g. the breast,  
CC thyroid, pancreas, uterus and kidneys.  
SQ Sequence 168 AA;

Query Match 100.0%; Score 892; DB 1; Length 168;  
Best Local Similarity 100.0%; Pred. No. 3.05e-77;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 103  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 60  
Db 104 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 163  
QY 61 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
Db 164 SOEQS 168  
QY 121 SOEQS 125

## RESULT 4

ID R85119 standard; Protein; 127 AA.

AC R85119;  
DT 01-MAR-1996 (first entry)  
DE Cell-cycle regulatory protein homologue.  
KW Cell-cycle regulatory protein; cyclin-dependent kinase inhibitor;  
KW CCR; cell proliferation; agonist; antagonist.  
OS Synthetic.

FH Key Location/Qualifiers  
FT misc\_difference 5. .7 /note= "unidentified amino acids"  
FT misc\_difference 10 /note= "unidentified amino acid"  
FT misc\_difference 14. .15 /note= "unidentified amino acids"  
FT misc\_difference 18. .19 /note= "unidentified amino acids"  
FT misc\_difference 22 /note= "unidentified amino acid"  
FT misc\_difference 25 /note= "unidentified amino acid"  
FT misc\_difference 27. .29 /note= "unidentified amino acids"  
FT misc\_difference 49. .50 /note= "unidentified amino acids"  
FT misc\_difference 65 /note= "unidentified amino acid"  
FT misc\_difference 69 /note= "unidentified amino acid"  
FT misc\_difference 71 /note= "unidentified amino acid"  
FT misc\_difference 74 /note= "unidentified amino acid"  
FT misc\_difference 76. .78 /note= "unidentified amino acids"  
FT misc\_difference 82 /note= "unidentified amino acid"  
FT misc\_difference 84 /note= "unidentified amino acid"  
FT W09528483-A1. /note= "unidentified amino acid"

PD 26-OCT-1995.  
PR 14-APR-1995; U04636.  
PR 14-APR-1994; US-227371.  
PR 25-MAY-1994; US-248812.  
PR 14-SEP-1994; US-306511.  
PR 29-NOV-1994; US-346147.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;  
FI WPI; 95-373798/48.



PT New cell cycle regulating proteins bind to cyclin dependent kinase -  
 PT and related nucleic acids, antibodies etc., used in diagnosis and  
 PT therapy of abnormal cell proliferation, degeneration etc.  
 PS Disclosure; Page 4; 109pp; English.  
 CC Cell-cycle regulatory (CCR) proteins (R85116-18, R85120) have the  
 CC general formula given in R85119. The CCR proteins specifically  
 CC bind to cyclin-dependent kinases and function as either agonists  
 CC or antagonists of cell cycle regulation.  
 SQ Sequence 127 AA;

Query Match 81.1%; Score 723; DB 1; Length 127;  
 Best Local Similarity 81.1%; Pred. No. 3.90e-60;  
 Matches 103; Conservative 0; Mismatches 22; Indels 2; Gaps 2;  
 Db 1 MMGMXXXVAXLLXGAXXNCXDPXTXXXPVHDAAREGFDTLVVHXGARDVWDAG 60  
 QY 1 MMGMNVHVAALLNYGADSNCEPTTFS-RPVHDAAREGFDTLVVHGGSGARDVWDAG 59  
 Db 61 GRLPXDLAYEXGHXXLYRXGCSLCSAGWSLCTAGNVAOTDGHSSSTPRALELR 120  
 QY 60 GRPLDLAQRGHQDIVRYLRSR-GCSLCSAGWSLCTAGNVAOTDGHSSSTPRALELR 118  
 Db 121 GQSQEQS 127  
 QY 119 GQSQEQS 125

RESULT 5  
 ID W80525 standard; Protein; 105 AA.  
 AC W80525;  
 DT 03-FEB-1999 (first entry)  
 DE A human multiple tumour suppressor 1E1-beta protein.  
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.  
 OS Homo sapiens.  
 PN US843756-A.  
 PD 01-DEC-1998.  
 PF 28-JUL-1995; 058735.  
 PR 28-JUL-1995; US-508735.  
 PR 07-JUN-1995; US-487033.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI Jiang P, Kamb A, Stone S;  
 DR WPI: 99-044585/04.  
 DR N-PSDB; V70594.  
 PT Mouse multiple tumour suppressor gene segment - useful for primer design  
 PS Example 8; Fig 12A-B; 80pp; English.  
 CC The present sequence represents human multiple tumour suppressor 1E1-beta  
 CC (MTS1E1-beta) protein. Primers designed from the gene can be used to  
 CC design primers to detect abnormalities i.e. polymorphisms which may  
 CC predispose towards malignancies such as melanoma, leukaemia,  
 CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,  
 CC thyroid, pancreas, uterus and kidneys.  
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 MMGMARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVHAGARDVWDAG 60  
 QY 1 MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVHGGSGARDVWDAG 60  
 Db 61 RLPVDLAEEIGHEDVARYLRAAA 83  
 QY 61 RLPDLAQRGHQDIVRYLRSAG 83

RESULT 6  
 ID R81700 standard; Protein; 105 AA.  
 AC R81700;  
 DT 08-MAY-1996 (first entry)  
 DE Multiple tumour suppressor 1 exon 1 beta (MTS1E1beta) polypeptide.  
 KW Multiple tumour suppressor; MTS1E1beta; cancer; diagnosis; assay;

KW predisposition; melanoma; leukaemia; lymphoma; prognosis;  
 KW pancreas; breast; thyroid; exon 1.  
 OS Homo sapiens.  
 PN WO9525813-A1.  
 PD 28-SEP-1995.  
 PF 17-MAR-1995; U03537.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215087.  
 PR 18-MAR-1994; US-215086.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR (MYRI-) MYRIAD GENETICS INC.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 PI Cannon-Albright LA, Kamb A, Skolnick MH;  
 DR WPI: 95-344626/44.  
 DR N-PSDB; T00744.  
 PT Detecting polymorphism associated with cancer pre-disposition - also  
 PT DNA, vectors and host cells e.g. for gene or protein replacement  
 PT therapy and drug screening  
 PS Example 7; Page 101; 148pp; English.  
 CC An individual can be diagnosed as having a predisposition to cancer  
 CC by detecting an alteration in the wild type multiple tumour  
 CC suppressor (MTS) gene, using gene probes which hybridise to the  
 CC MTS1E1beta gene ORF T00744 (which encodes R81700). The above assay  
 CC can also be used in the diagnosis and prognosis of melanoma,  
 CC lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.  
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 MMGMARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVHAGARDVWDAG 60  
 QY 1 MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVHGGSGARDVWDAG 60  
 Db 61 RLPVDLAEEIGHEDVARYLRAAA 83  
 QY 61 RLPDLAQRGHQDIVRYLRSAG 83

RESULT 7  
 ID W74550 standard; Protein; 105 AA.  
 AC W74550;  
 DT 04-DEC-1998 (first entry)  
 DE Amino acid sequence 1 of the multiple tumour suppressor MTS1E1S.  
 KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;  
 KW somatic mutation; gene therapy.  
 OS Homo sapiens.  
 PN US5801236-A.  
 PD 01-SEP-1998.  
 PF 07-JUN-1995; 480810.  
 PR 07-JUN-1995; US-480810.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03316.  
 PR (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR WPI: 98-494842/42.  
 DR N-PSDB; V53830.  
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
 PT useful as hybridisation probes, primers and recombinant production  
 PT of MTS in the diagnosis and treatment of cancers related to MTS  
 PT mutation(s)  
 PS Example 7; Column 75-76; 73pp; English.  
 CC This is the amino acid sequence of the multiple tumour suppressor  
 CC (MTS1E1S) protein, used in the method of the invention. The MTS gene  
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
 CC standard nucleic hybridisation techniques, of patient samples. The  
 CC mutated sequences are those that are present in somatic mutations

CC of the gene in cancers. The vectors can be used for gene therapy  
 CC strategies to replace function of mutated protein in patients. These  
 CC can also be used to construct protein mimetics, also for therapeutic  
 CC strategies. In addition the expression constructs can also be used  
 CC for recombinant production of MTS. Recombinant MTS can be used to  
 CC screen for drugs to be used for cancer therapy, and the protein  
 CC itself may also be used to restore MTS function in a cell.  
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 MMGSGARVAELLLHGAEPNCADPATLTPVHDAAREGFLDTLVLRAGARLDVRDANG 60  
 QY 1 MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60  
 Db 61 RLPVDLAEELGHRDVARYLRAAA 83  
 QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

RESULT 8  
 ID R80947 standard; Protein; 105 AA.  
 AC R80947;  
 DT 03-MAY-1996 (first entry)  
 DE Human multiple tumour suppressor polypeptide, MTS1E1-beta.  
 KW Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;  
 KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;  
 KW gene therapy; chronic.  
 OS Homo sapiens.  
 PN WO9525429-A1.  
 PD 28-SEP-1995.  
 PF 17-MAR-1995; U03316.  
 PR 18-MAR-1994; US-214581.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR WPI; 95-344401/44.  
 DR N-PSDB; Q99164.  
 PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences  
 PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.  
 PT melanoma or leukaemia

PS Claim 5; Page 101; 156pp; English.  
 CC Several multiple tumour suppressor (MTS) polypeptides have been isolated  
 CC and sequenced. This sequence is the MTS polypeptide MTS1E1-beta.  
 CC MTS polypeptide-encoding cDNAs and mutants of these are useful for  
 CC the diagnosis or prognosis of human cancer. Germ-line mutations of  
 CC MTS cDNAs can be used for diagnosing predisposition to melanoma,  
 CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's  
 CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,  
 CC testis, kidney, stomach and rectum. The wild-type gene is useful  
 CC for gene therapy and MTS polypeptides may also be used for protein  
 CC replacement therapy. Also the polypeptides or cells contg. an  
 CC altered MTS gene are useful for screening for potential cancer  
 CC therapeutics.  
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 MMGSGARVAELLLHGAEPNCADPATLTPVHDAAREGFLDTLVLRAGARLDVRDANG 60  
 QY 1 MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60  
 Db 61 RLPVDLAEELGHRDVARYLRAAA 83  
 QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

QY 61 RLPLDLAQERGHQDIVRYLRSAG 83  
 RESULT 9  
 ID W19254 standard; Protein; 105 AA.  
 AC W19254;  
 DT 10-SEP-1997 (first entry)  
 DE Human multiple tumour suppressor 1 Elbeta gene product.  
 KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;  
 KW Elbeta.  
 OS Homo sapiens.  
 PN US5624819-A.  
 PD 29-APR-1997.  
 PF 18-MAR-1994; 214582.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03537.  
 PR 07-JUN-1995; US-474177.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI (UTAH) UNIV UTAH RES FOUND.  
 PI Cannon-Albright LA, Kamb A, Skolnick MH;  
 DR WPI; 97-258217/23.  
 DR N-PSDB; T69780.  
 PT Human mutant multiple tumour suppressor gene sequences - for  
 PT production of recombinant mutant polypeptide(s)  
 PS Disclosure: Columns 73-74; 72pp; English.  
 CC The present sequence the human multiple tumour suppressor 1  
 CC (MTS1) Elbeta gene product, useful in cancer diagnosis.  
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 MMGSGARVAELLLHGAEPNCADPATLTPVHDAAREGFLDTLVLRHSGARLDVRDANG 60  
 QY 1 MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60  
 Db 61 RLPVDLAEELGHRDVARYLRAAA 83  
 QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

RESULT 10  
 ID W40525 standard; Protein; 105 AA.  
 AC W40525;  
 DT 15-JUL-1998 (first entry)  
 DE Human MTS1E1-beta protein.  
 KW MTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;  
 KW germ-line mutation; familial melanoma locus; MLM; predisposition.  
 OS Homo sapiens.  
 PN US5739027-A.  
 PD 14-APR-1998.  
 PF 07-JUN-1995; 487033.  
 PR 07-JUN-1995; US-487033.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03316.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR WPI; 98-250421/22.  
 DR N-PSDB; V11249.  
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are  
 PT useful for the diagnosis of cancers related to MTS1E1-beta  
 PT mutation(s) and their treatment  
 PS Claim 1; Fig 12; 72pp; English.  
 CC This sequence represents a human multiple tumour suppression protein,



CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a  
 CC locus activated by translocation to an immunoglobulin gene enhancer  
 CC in some B-cell lymphomas and leukemias. D-type cyclin, cyclin  
 CC dependent kinase (CDK), PCNA (proliferating cell nuclear antigen) and  
 CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many  
 CC combinatorial variations of the components e.g. cyclin D1 or D3 and  
 CC CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may  
 CC have a subtle different role in the cell cycle or in different cell  
 CC types. Cellular transformation by DNA tumour viruses such as SV40  
 CC is associated with selective subunit rearrangement of the cyclin D  
 CC complexes. In virally transformed cells, CDK4 totally dissociates  
 CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton  
 CC polypeptide (p16). This sequence, designated p16INK4, binds to and  
 CC inhibits CDK4. p16INK4 was discovered to show many similarities to  
 CC p16. Reagents, such as monoclonal antibodies, can be developed that  
 CC recognise the interactions between the CDK's cyclins, PCNA and low  
 CC molecular weight polypeptides and can therefore be used to identify  
 CC the state of transformation of a cell.  
 SQ Sequence 151 AA;

Query Match 53.0%; Score 473; DB 1; Length 151;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 44 MMGSGARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVRDANG 103  
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLRHSGARLDVRDANG 60  
 Db 104 RLPVDLAELGHRDVARYLRAA 126  
 QY 61 RLPDLAQERGHODIVRYLRSAG 83

RESULT 14  
 ID W74549 standard; Protein; 156 AA.  
 AC W74549;  
 DT 04-DEC-1998 (first entry)  
 DE Amino acid sequence of multiple tumour suppressor 1.  
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;  
 KW somatic mutation; gene therapy.  
 OS Homo sapiens.  
 PN US5801236-A.  
 PD 01-SEP-1998.  
 PF 07-JUN-1995; 480810.  
 PR 07-JUN-1995; US-480810.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-003316.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR N-PSDB; V53819.  
 DR N-PSDB; V53819.  
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
 PT useful as hybridisation probes, primers and recombinant production  
 PT of MTS in the diagnosis and treatment of cancers related to MTS  
 PT mutation(s)  
 PS Disclosure: Column 63-64; 73pp; English.

CC This is the amino acid sequence of the multiple tumour suppressor 1  
 CC (MTS-1) protein, used in the method of the invention. The MTS gene  
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
 CC standard nucleic hybridisation techniques, of patient samples. The  
 CC mutated sequences are those that are present in somatic mutations  
 CC of the gene in cancers. The vectors can be used for gene therapy  
 CC strategies to replace function of mutated protein in patients. These  
 CC can also be used to construct protein mimetics, also for therapeutic  
 CC strategies. In addition the expression constructs can also be used  
 CC for recombinant production of MTS. Recombinant MTS can be used to  
 CC screen for drugs to be used for cancer therapy, and the protein  
 CC itself may also be used to restore MTS function in a cell.  
 SQ Sequence 156 AA;

Query Match 53.0%; Score 473; DB 1; Length 156;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 52 MMGSGARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVRDANG 111  
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLRHSGARLDVRDANG 60  
 Db 112 RLPVDLAELGHRDVARYLRAA 134  
 QY 61 RLPDLAQERGHODIVRYLRSAG 83

RESULT 15  
 ID R85116 standard; Protein; 156 AA.  
 AC R85116;  
 DT 01-MAR-1996 (first entry)  
 DE Cell-cycle regulatory protein p16.  
 KW Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;  
 KW CCR; cancer; cell proliferation.  
 OS Homo sapiens.  
 PN WQ9528483-A1.  
 PD 26-OCT-1995.  
 PF 14-APR-1995; U04636.  
 PR 14-APR-1994; US-227371.  
 PR 25-MAY-1994; US-248812.  
 PR 14-SEP-1994; US-306511.  
 PR 29-NOV-1994; US-346147.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;  
 DR WPI; 95-373798/48.  
 DR N-PSDB; T02962.  
 PT New cell cycle regulating proteins bind to cyclin dependent kinase -  
 PT and related nucleic acids, antibodies etc., used in diagnosis and  
 PT therapy of abnormal cell proliferation, degeneration etc.  
 PS Claim 1; Page 76-77; 109pp; English.

CC The human cell-cycle regulatory (CCR) protein p16 (R85116) was  
 CC obtd. by expression of a cDNA clone (T02962) isolated in a 2-hybrid  
 CC screening assay. CCR p16 specifically inhibits the activity of  
 CC cyclin-dependent kinases during various stages of the cell cycle,  
 CC and can be used in the treatment and diagnosis of proliferative  
 CC disorders.  
 CC Sequence 156 AA;

Query Match 53.0%; Score 473; DB 1; Length 156;  
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;  
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 52 MMGSGARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVRDANG 111  
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLRHSGARLDVRDANG 60  
 Db 112 RLPVDLAELGHRDVARYLRAA 134  
 QY 61 RLPDLAQERGHODIVRYLRSAG 83

Search completed: Thu Jul 20 08:41:38 2000  
 Job time : 9 secs.

\*\*\*\*\*  
M P S R E L H (TM)  
\*\*\*\*\*  
Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Jul 20 08:43:29 2000; MasPar time 5.20 Seconds  
347.144 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-016-869A-6  
Description: (1-125) from US09016869A.pap  
Perfect Score: 892  
Sequence: 1 MMGNVHVAALLLTGADSN.....SFSSSTPRALRLRGQSQEQS 125

Scoring table: PAM 150  
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfiles1

Statistics: Mean 28.127; Variance 120.872; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Length	ID	Description	Pred. No.
1	892	100.0	125	4 PCT-US95-0 Sequence 6, Applicatio	2.41e-75
2	892	100.0	125	2 US-08-306- Sequence 6, Applicatio	2.41e-75
3	892	100.0	125	2 US-08-893- Sequence 6, Applicatio	2.41e-75
4	892	100.0	125	2 US-08-954- Sequence 5, Applicatio	2.41e-75
5	892	100.0	125	3 US-08-581- Sequence 6, Applicatio	2.41e-75
6	892	100.0	125	1 US-08-534- Sequence 5, Applicatio	2.41e-75
7	892	100.0	167	2 US-08-627- Sequence 6, Applicatio	2.41e-75
8	892	100.0	168	2 US-08-508- Sequence 14, Applicati	9.07e-59
9	723	81.1	127	3 US-08-581- Sequence 39, Applicati	7.98e-49
10	621	69.6	85	3 US-08-581- Sequence 38, Applicati	1.62e-34
11	473	53.0	88	3 US-08-581- Sequence 37, Applicati	1.62e-34
12	473	53.0	89	3 US-08-581- Sequence 14, Applicati	1.62e-34
13	473	53.0	105	3 US-09-120- Sequence 14, Applicati	1.62e-34
14	473	53.0	105	2 US-08-486- Sequence 14, Applicati	1.62e-34
15	473	53.0	105	1 US-08-474- Sequence 14, Applicati	1.62e-34
16	473	53.0	105	2 US-08-508- Sequence 14, Applicati	1.62e-34
17	473	53.0	105	1 US-08-480- Sequence 14, Applicati	1.62e-34
18	473	53.0	105	2 US-08-848- Sequence 14, Applicati	1.62e-34
19	473	53.0	105	1 US-08-487- Sequence 14, Applicati	1.62e-34
20	473	53.0	148	4 PCT-US93-0 Sequence 4, Applicatio	1.62e-34
21	473	53.0	148	1 US-08-154- Sequence 4, Applicatio	1.62e-34
22	473	53.0	148	3 US-08-384- Sequence 16, Applicati	1.62e-34
23	473	53.0	148	3 US-08-384- Sequence 24, Applicati	1.62e-34

24	473	53.0	156	4 PCT-US95-0 Sequence 2, Applicatio	1.62e-34
25	473	53.0	156	3 US-08-581- Sequence 2, Applicatio	1.62e-34
26	473	53.0	156	3 US-09-120- Sequence 2, Applicatio	1.62e-34
27	473	53.0	156	2 US-08-627- Sequence 2, Applicatio	1.62e-34
28	473	53.0	156	2 US-08-306- Sequence 2, Applicatio	1.62e-34
29	473	53.0	156	2 US-08-486- Sequence 2, Applicatio	1.62e-34
30	473	53.0	156	2 US-08-508- Sequence 2, Applicatio	1.62e-34
31	473	53.0	156	1 US-08-474- Sequence 2, Applicatio	1.62e-34
32	473	53.0	156	2 US-08-848- Sequence 2, Applicatio	1.62e-34
33	473	53.0	156	1 US-08-480- Sequence 2, Applicatio	1.62e-34
34	473	53.0	156	2 US-08-893- Sequence 2, Applicatio	1.62e-34
35	473	53.0	156	1 US-08-487- Sequence 2, Applicatio	1.62e-34
36	473	53.0	391	1 US-08-589- Sequence 2, Applicatio	1.62e-34
37	472	52.9	136	4 PCT-US95-0 Sequence 6, Applicatio	2.02e-34
38	472	52.9	137	2 US-08-306- Sequence 4, Applicatio	2.02e-34
39	472	52.9	137	2 US-08-893- Sequence 4, Applicatio	2.02e-34
40	472	52.9	138	4 PCT-US95-0 Sequence 16, Applicati	2.02e-34
41	472	52.9	138	1 US-08-480- Sequence 16, Applicati	2.02e-34
42	472	52.9	138	3 US-09-120- Sequence 16, Applicati	2.02e-34
43	472	52.9	138	1 US-08-474- Sequence 16, Applicati	2.02e-34
44	472	52.9	138	2 US-08-627- Sequence 4, Applicatio	2.02e-34
45	472	52.9	138	1 US-08-487- Sequence 16, Applicati	2.02e-34

ALIGNMENTS

RESULT 1  
ID PCT-US95-04636-6 STANDARD; PRT; 125 AA.  
XX  
AC  
XX  
XX  
DT

Sequence 6, Application PC/TUS9504636

Sequence 6, Application PC/TUS9504636

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

TITLE OF INVENTION: Related Thereto

NUMBER OF SEQUENCES: 10

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Ascii(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04636

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/346,147

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/306,511

FILING DATE: 14-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,812

FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,371

FILING DATE: 14-APR-1994

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 125 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 4; Length 125;

Best Local Similarity 100.0%; Pred. No. 2.41e-75;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



SQ SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2.41e-75;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLHGSGARLDVDRDAG 60  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLHGSGARLDVDRDAG 60  
Db 61 RLPLDLAQRGHODIVYRLSAGCSLCSAGWSLCTAGNVAQTGDHGSFSSSTPRALELRGQ 120  
QY 61 RLPLDLAQRGHODIVYRLSAGCSLCSAGWSLCTAGNVAQTGDHGSFSSSTPRALELRGQ 120  
Db 121 SEQOS 125  
QY 121 SEQOS 125

RESULT 4  
ID US-08-954-470-5 STANDARD; PRT; 125 AA.  
AC xxxxxx  
DE DE  
DT DT  
XX XX  
XX XX

Sequence 5, Application US/08954470

Sequence 5, Application US/08954470  
Patent No. 5876965  
GENERAL INFORMATION:  
APPLICANT: Sherr, Charles, J.  
APPLICANT: Quelle, Dawn, E.  
TITLE OF INVENTION: ARE-p19, A No. 5876965el Regulator of the  
TITLE OF INVENTION: Mammalian Cell Cycle  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/954,470  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/534,975  
FILING DATE: 28-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fox, Samuel, L.  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0656.0590000  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2.41e-75;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLHGSGARLDVDRDAG 60  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLHGSGARLDVDRDAG 60  
Db 61 RLPLDLAQRGHODIVYRLSAGCSLCSAGWSLCTAGNVAQTGDHGSFSSSTPRALELRGQ 120  
QY 61 RLPLDLAQRGHODIVYRLSAGCSLCSAGWSLCTAGNVAQTGDHGSFSSSTPRALELRGQ 120  
Db 121 SEQOS 125  
QY 121 SEQOS 125

RESULT 5  
ID US-08-581-918A-6 STANDARD; PRT; 125 AA.  
AC xxxxxx  
DE DE  
DT DT  
XX XX  
XX XX

Sequence 6, Application US/08581918A

Sequence 6, Application US/08581918A  
Patent No. 6043030  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Thereto  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/581,918A  
FILING DATE: 02-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/497,214  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/346,147  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709

CC REFERENCE/DOCKET NUMBER: MIV-071.06  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (617) 832-1299  
CC TELEFAX: (617) 832-7000  
CC INFORMATION FOR SEQ ID NO: 6:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 125 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 3; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2,41e-75;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNTYGADSNCEDPITFSRPVHDAAREGFELDTLVVLHGSGARLDVWDWG 60  
QY 1 MMGNVHVAALLNTYGADSNCEDPITFSRPVHDAAREGFELDTLVVLHGSGARLDVWDWG 60

Db 61 RLPLDLAQRGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
QY 61 RLPLDLAQRGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120

Db 121 SEQES 125  
QY 121 SEQES 125

RESULT 6  
ID US-08-534-975-5 STANDARD; PRT; 125 AA.

XX  
AC  
XX  
XX  
DT  
XX  
XX

Sequence 5, Application US/08534975

Sequence 5, Application US/08534975

Patent No. 5723313

GENERAL INFORMATION:

APPLICANT: Sherr, Charles, J.

APPLICANT: Quelle, Dawn, E.

TITLE OF INVENTION: ANF-p19, A No. 5723313el Regulator of the Mammalian Cell

TITLE OF INVENTION: Cycle

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,975

FILING DATE: 28-SEP-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel, L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656.0590000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 125 amino acids

TYPE: amino acid

CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 1; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2,41e-75;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNTYGADSNCEDPITFSRPVHDAAREGFELDTLVVLHGSGARLDVWDWG 60  
QY 1 MMGNVHVAALLNTYGADSNCEDPITFSRPVHDAAREGFELDTLVVLHGSGARLDVWDWG 60

Db 61 RLPLDLAQRGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
QY 61 RLPLDLAQRGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120

Db 121 SEQES 125  
QY 121 SEQES 125

RESULT 7  
ID US-08-627-610-6 STANDARD; PRT; 167 AA.

XX  
AC  
XX  
XX  
DT  
XX  
XX

Sequence 6, Application US/08627610

Sequence 6, Application US/08627610

Patent No. 5919997

GENERAL INFORMATION:

APPLICANT: Beach, David H.

APPLICANT: Serrano, Manuel

APPLICANT: Depinho, Ronald A.

TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle

TITLE OF INVENTION: Regulation

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/627,610

FILING DATE: 04-APR-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: CSI-001CP6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 167 AA; 17870 MW; 131634 CN;

Query Match 100.0%; Score 892; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2,41e-75;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Db	103	RLPLDLAQRGHODIVRYLSAGCSLCSAGWSLCTAGNVAQTGDGHSFSSSTPRALELRGO	162
Qy	61	RLPLDLAQRGHODIVRYLSAGCSLCSAGWSLCTAGNVAQTGDGHSFSSSTPRALELRGO	120
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Qy	121	SQEQS 125	
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AC	xxxxxx		
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CC	Sequence 46, Application US/08508735		
CC	Sequence 46, Application US/08508735		
CC	Patent No. 5843756		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Stone, Steven		
CC	APPLICANT: Jiang, Ping		
CC	APPLICANT: Kamb, Alexander		
CC	TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF		
CC	NUMBER OF SEQUENCES: 47		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP		
CC	STREET: 1201 New York Avenue, Suite 1000		
CC	CITY: Washington		
CC	STATE: DC		
CC	COUNTRY: USA		
CC	ZIP: 20005		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/508,735		
CC	FILING DATE:		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US to be assigned		
CC	FILING DATE: 07-JUN-1995		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: PCT/US95/03316		
CC	FILING DATE: 17-MAR-1995		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Ihnen, Jeffrey L.		
CC	REGISTRATION NUMBER: 28,957		
CC	REFERENCE/DOCKET NUMBER: 24884-109348		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 202-962-4848		
CC	TELEFAX: 202-962-8300		
CC	INFORMATION FOR SEQ ID NO: 46:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 168 amino acids		
CC	TYPE: amino acid		
CC	STRANDEDNESS: single		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
CC	HYPOTHETICAL: NO		
CC	ORIGINAL SOURCE:		
CC	ORGANISM: Mus musculus		
CC	SEQUENCE 168 AA; 17901 MW; 133219 CN;		
SO			
Query Match	100.0%; Score 892;	DB 2: Length 168;	

[illegible]









\*\*\*\*\*  
MPSREH  
(TM)  
\*\*\*\*\*  
Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd  
Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Jul 20 08:41:56 2000; MspPar time 10.59 Seconds  
Tabular output not generated.  
556.609 Million cell updates/sec

Title: >US-09-016-869A-6  
Description: (1-125) from US09016869A.pep  
Perfect Score: 892  
Sequence: 1 MMGNVHVAALLNYGADSN.....SFSSSTPRALELRGQSSEQS 125  
Scoring table: PAM 150  
Gap 11  
Searched: 142080 seqs, 47172406 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: pir63  
1:pir1 2:pir2 3:pir3 4:pir4  
Statistics: Mean 41.141; Variance 75.478; scale 0.545  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Length	DB ID	Description	Pred. No.		
1	892	100.0	167	2	I58352	pl6INK4a - mouse	2.02e-169
2	473	53.0	156	2	JE0141	cyclin dependent kina	4.04e-76
3	472	52.9	138	2	B55479	CDK4 inhibitor p14(IN	6.66e-76
4	461	51.7	130	2	I78845	pl5INK4b - mouse	1.62e-73
5	233	26.1	164	2	A57378	cyclin-dependent kina	7.47e-26
6	228	25.6	41	2	I52720	gene pl5INK4B protein	7.19e-25
7	218	24.4	166	2	B57378	cyclin-dependent kina	6.47e-23
8	218	24.2	166	2	A57379	CDK4/CDK6 inhibitor p	6.47e-23
9	198	22.2	168	2	B57379	CDK4/CDK6 inhibitor p	4.56e-19
10	193	21.6	168	2	A55479	CDK6 inhibitor p18 -	4.05e-18
11	156	17.5	2531	2	S18198	notch protein homolog	2.58e-11
12	154	17.3	2555	2	A40043	notch protein homolog	5.86e-11
13	149	16.7	2531	2	A46019	Notch-1 protein - mou	4.46e-10
14	148	16.6	638	2	A56695	Notch2 protein homolo	6.67e-10
15	148	16.6	2471	2	A49128	cell-fate determining	6.67e-10
16	147	16.5	2318	2	S45306	notch 3 protein - mou	9.97e-10
17	147	16.5	2321	2	S78549	notch3 protein - huma	9.97e-10
18	146	16.4	2437	2	S42612	transmembrane protein	1.49e-09
19	140	15.7	3924	2	S37431	ankyrin 2, neuronal 1	1.62e-08
20	138	15.5	1423	1	I37275	death-associated prot	3.56e-08
21	138	15.5	2524	2	A35844	Xotch protein - Afric	3.56e-08
22	136	15.2	1848	2	S37711	ankyrin, erythrocyte	7.79e-08
23	136	15.2	1856	2	B35049	ankyrin 1, erythrocyt	7.79e-08

24	136	15.2	1862	2	I49502	ankyrin - mouse	7.79e-08
25	136	15.2	1880	2	A35049	ankyrin 1, erythrocyt	7.79e-08
26	136	15.2	1881	1	SJHUK	ankyrin 1, erythrocyt	7.79e-08
27	133	14.9	1549	2	T13940	ankyrin - fruit fly (	2.50e-07
28	131	14.7	1411	2	S30355	alpha-latroinsectox	5.41e-07
29	130	14.6	4377	2	A55755	ankyrin 3, long splic	7.94e-07
30	129	14.5	1786	2	A57282	ankyrin-related prote	1.16e-06
31	129	14.5	1809	2	T15345	ankyrin-related unc-4	1.16e-06
32	129	14.5	1815	2	T15346	elegans ankyrin-relat	1.16e-06
33	129	14.5	1867	2	T15344	ankyrin-related unc-4	1.16e-06
34	129	14.5	2039	2	T15347	ankyrin-related unc-4	1.16e-06
35	124	13.9	209	2	T15888	hypothetical protein	7.74e-06
36	120	13.5	1401	2	S11527	alpha-latrotoxin prec	3.44e-05
37	119	13.3	2703	1	A24420	notch protein - fruit	4.98e-05
38	116	13.0	334	2	T09017	probable acyl-CoA bin	1.50e-04
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43	109	12.2	500	2	A44369	ankyrin repeat acidic	1.85e-03
44	108	12.1	201	2	F64758	yand protein - Escher	2.63e-03
45	105	11.8	1436	2	S57238	forked protein 5.4K -	7.49e-03

ALIGNMENTS

RESULT 1  
ENTRY I58352 #type complete  
TITLE pl6INK4a - mouse  
ORGANISM #formal\_name Mus sp. #common\_name mouse  
DATE 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 28-Feb-1997  
ACCESSIONS I58352  
REFERENCE I58352  
#authors Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr, C.J.; Serrano, M.  
#journal Oncogene (1995) 11:635-645  
#title Cloning and characterization of murine pl6INK4a and pl5INK4b genes.  
#cross-references MUID:95380169  
#accession I58352  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
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#cross-references GB:S79251; NID:g1087090; PID:g1087091  
GENETICS  
#gene pl6INK4a  
SUMMARY #length 167 #molecular-weight 17870 #checksum 1257

Query Match 100.0%; Score 892; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2.02e-169;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 43 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVRDANG 102  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVRDANG 60  
Db 103 RLPLDLAQERGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTPRALELRGQ 162  
QY 61 RLPLDLAQERGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTPRALELRGQ 120  
Db 163 SEQES 167  
QY 121 SEQES 125

RESULT 2  
ENTRY JE0141 #type complete  
TITLE cyclin dependent kinase - human  
ALTERNATE\_NAMES CDK4 inhibitor pl6INK4a/MTS1; cyclin-dependent kinase inhibitor 2A; multiple tumor suppressor 1 (MTS1)  
ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change  
26-Aug-1999  
ACCESSIONS JE0141; I59268; S39359; I59585; JC5679  
REFERENCE JE0141  
#authors Huang, C.G.; Deng, W.; Fu, J.L.  
#journal Chinese J. Biotechnol. (1997) 13:105-107  
#title Molecular cloning and sequencing of p16ink4 cDNA from hela cell.  
#accession JE0141  
#molecule\_type mRNA  
#residues 1-156 #label HUA  
#experimental\_source Hella cell  
REFERENCE I59268  
#authors Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, W.P.; Forrester, K.; Gerwin, B.; Serrano, M.; Beach, D.H.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:11045-11049  
#title Mutations and altered expression of p16INK4 in human cancer.  
#cross-references MUID:95062202  
#accession I59268  
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#molecule\_type DNA  
#residues 1-152 #label RES  
#cross-references GB:S74232; NID:9710467  
#note this report is a correction  
REFERENCE S39359  
#authors Serrano, M.; Hannon, G.J.; Beach, D.  
#journal Nature (1993) 366:704-707  
#title A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.  
#cross-references MUID:94081956  
#accession S39359  
#status preliminary  
#molecule\_type mRNA  
#residues 9-34,'V',36-156 #label SER  
#note this sequence has been corrected in reference I59268  
REFERENCE I59585  
#authors Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.; Johnson, B.E.; Skolnick, M.H.  
#journal Science (1994) 264:436-440  
#title A cell cycle regulator potentially involved in genesis of many tumor types.  
#cross-references MUID:94204645  
#accession I59585  
#status translation not shown; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 51-152 #label RE2  
#cross-references GB:S69804; NID:9546272  
REFERENCE JC5679  
#authors Huang, C.; Deng, W.; Fu, J.  
#journal Chinese J. Biotechnol. (1997) 13:105-107  
#title Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
#accession JC5679  
#molecule\_type mRNA  
#residues 1-156 #label HU2  
COMMENT This protein suppresses the function of cyclin D1/CDK4 and cyclin D1/CDK6.  
GENETICS  
#gene p16ink4; MIM; CDKN2; MTS1  
#cross-references GDB:335362; GDB:CDKN2A; OMIM:600160  
#map\_position 9p21-9p21  
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins  
KEYWORDS cell cycle control; protein kinase inhibitor; tumor suppressor  
SUMMARY #length 156 #molecular-weight 16532 #checksum 6490  
Query Match 53.0%; Score 473; DB 2; Length 156;  
Best Local Similarity 73.5%; Pred. No. 4.04e-76;  
Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
Db 52 MMGSGARVAELLLHGAPNCADPATLRPVHDAAREGFLDTLVVLRAGARLDVRDAG 111

QY 1 MMGNVHVAAALNTGADSCNDPTFSRPHVDAAREGFLDTLVVLRAGARLDVRDAG 60  
Db 112 RLPLVLAELGHRDVARVYRAAA 134  
QY 61 RLPLDLAQRGHQDVRVYLRAG 83  
RESULT 3  
ENTRY B55479 #type complete  
TITLE CDK4 inhibitor p14(INK4B/MTS2) - human  
ALTERNATE\_NAMES CDK6-associated protein p15(INK4B); cyclin-dependent kinase inhibitor 2B; multiple tumor suppressor 2  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 28-May-1999  
ACCESSIONS B55479; S47593; I81183; I52713  
REFERENCE A55479; S47593; I81183; I52713  
#authors Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Xiong, Y.  
#journal Genes Dev. (1994) 8:2939-2952  
#title Growth suppression by p18, a p16(INK4/MTS1)- and p14(INK4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRB function.  
#cross-references MUID:95095079  
#accession B55479  
#molecule\_type mRNA  
#residues 1-138 #label GUA  
#cross-references GB:U17075; NID:9639715; PID:9639716  
#experimental\_source HeLa cells  
REFERENCE S47593  
#authors Hannon, G.J.; Beach, D.  
#journal Nature (1994) 371:257-261  
#title p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.  
#cross-references MUID:94359613  
#accession S47593  
#molecule\_type mRNA  
#residues 1-19,'TP',22,24-31,'HSW',35-138 #label HAN  
#cross-references GB:I36844; NID:9556197; PIDN:AAA50282.1; PID:9556198  
#experimental\_source HaCat cells  
REFERENCE I59585  
#authors Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.; Johnson, B.E.; Skolnick, M.H.  
#journal Science (1994) 264:436-440  
#title A cell cycle regulator potentially involved in genesis of many tumor types.  
#cross-references MUID:94204645  
#accession I81183  
#status translation not shown; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 53-138 #label KAM  
#cross-references GB:S69805; NID:9546273  
REFERENCE I52713  
#authors Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler, K.W.; Vogelstein, B.  
#journal Cancer Res. (1994) 54:6353-6358  
#title Deletion of p16 and p15 genes in brain tumors.  
#cross-references MUID:95079408  
#accession I52713  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 1-52 #label RES  
#cross-references GB:S75756; NID:9861470  
GENETICS  
#gene GDB:CDKN2B; MTS2  
#cross-references GDB:579577; OMIM:600431  
#map\_position 9p21-9p21  
KEYWORDS cell cycle control; protein kinase inhibitor; tumor suppressor  
SUMMARY #length 138 #molecular-weight 14722 #checksum 1236



SUMMARY	#length 164	#molecular-weight 17362	#checksum 5271
Query Match	26.1%	Score 233;	DB 2; Length 164;
Best Local Similarity	46.5%	Pred. No. 7.47e-25;	
Matches	40; Conservative	15; Mismatches 29;	Indels 2; Gaps 2;
Db	48	MMEGSAIALELLKOGASPNVDTSG-TSPVHDAARGFGLDTLKLVIYEHGADVNPDPGTG	106
Qy	1	MMMGNVHVAALLNYGADNSCEDPTTFSPRVHDAAREGFGLDTLVVHSGARLDRDPAWG	60
Db	107	ALPIHLAVQEGHTVVSFL-AAESDL	131
Qy	61	RLPLDLAQERGHQDIVRYLSAGCSL	86
RESULT	6		
ENTRY		I52720	#type fragment
TITLE		gene p15INK4B protein - rat (fragment)	
ORGANISM		#formal_name Rattus sp. #common_name rat	
DATE		26-Jul-1996 #sequence_revision 26-Jul-1996	#text_change
ACCESSIONS		28-Feb-1997	
REFERENCE		I52720	
#authors		Knappek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.	
#journal		Cancer Res. (1995) 55:1607-1612	
#title		Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors.	
#cross-references		MUID:95228036	
#accession		I52720	
#status		preliminary;	translated from GB/EMBL/DBJ
#molecule_type		DNA	
#residues		1-41	#label RES
#cross-references		GB:S77734; NID:G998711	
GENETICS			
#gene		p15INK4B	
SUMMARY		#length 41	#checksum 3296
Query Match	25.6%	Score 228; DB 2; Length 41;	
Best Local Similarity	70.7%	Pred. No. 7.19e-25;	
Matches	29; Conservative	7; Mismatches 5;	Indels 0; Gaps 0;
Db	1	MMGSAQVAELLLHGAEPNCADPATLTRPVHDAAREGFGLD	41
Qy	1	MMMGNVHVAALLNYGADNSCEDPTTFSPRVHDAAREGFGLD	41
RESULT	7		
ENTRY		B57378	#type complete
TITLE		cyclin-dependent kinase inhibitor p19 - mouse	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		08-Feb-1996 #sequence_revision 08-Feb-1996	#text_change
ACCESSIONS		20-Sep-1999	
REFERENCE		B57378	
#authors		Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.	
#journal		Mol. Cell. Biol. (1995) 15:2682-2688	
#title		Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to p16(Ink4).	
#cross-references		MUID:95257949	
#accession		B57378	
#status		preliminary	
#molecule_type		mRNA	
#residues		1-166	#label CHA
#cross-references		GB:U20497; NID:G791204; PIDN:AA085437.1; PID:G791205	
CLASSIFICATION		#superfamily unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology	
SUMMARY		#length 166	#molecular-weight 17920 #checksum 3767
Query Match	24.4%	Score 218; DB 2; Length 166;	
Best Local Similarity	48.1%	Pred. No. 6.47e-23;	
Matches	38; Conservative	13; Mismatches 27;	Indels 1; Gaps 1;

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Db 45 MKLGNPEIARLLLR-GANPNLKDGTGFA-VIHDAAARGFDTTQTLLEFQADVNIEDNE 102
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Qy 1 MAMGNVHVA-LLNLTGADSNCEDTTFSRPVHDAAREGFDTTLVVLHGSGARLDVRDAW 59
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Db 103 GNPLHLAAKEGHLPVVEFLMKHTACNV 130
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Qy 60 GRUPLDLAQRGHQDIVRYL-RSAGCSL 86
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |

RESULT 10
ENTRY A55479 #type complete
TITLE CDK6 inhibitor p18 ~ human
ALTERNATE_NAMES cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
kinase CDK6 inhibitor p18
ORGANISM #formal_name Homo sapiens #common_name man
DATE 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
20-Sep-1999
ACCESSIONS A55479
REFERENCE A55479
#authors Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.;
O'Keefe, C.L.; Matera, A.G.; Xiong, Y.
#journal Genes Dev. (1994) 8:2939-2952
#title Growth suppression by p18, a p16(INK4/MTS1)- and p14
(INK4B/MTS2)-related CDK6 inhibitor, correlates with
wild-type pRB function.
#cross-references MUID:95095079
#accession A55479
#molecule_type mRNA
#residues 1-168 #label GUA
#cross-references GB:U17074; NID:9639713; PIDN:AAC50074.1; PID:g639714
GENETICS
#gene GDB:CDKN2C
#cross-references GDB:594931
#map_position lp32-lp32
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
KEYWORDS cell cycle control; protein kinase inhibitor; tumor
suppressor
SUMMARY #length 168 #molecular-weight 18127 #checksum 9379

Query Match 21.6%; Score 193; DB 2; Length 168;
Best Local Similarity 45.0%; Pred. No. 4,05e-16;
Matches 36; Conservative 13; Mismatches 28; Indels 3; Gaps 3;

Db 45 MKLGNPEIARLLLR-GANPNLKDGTGFA-VIHDAAARGFDTTQTLLEFQADVNIEDNE 102
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Qy 1 MAMGNVHVA-LLNLTGADSNCEDTTFSRPVHDAAREGFDTTLVVLHGSGARLDVRDAW 59
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Db 103 GNPLHLAAKEGHLRVVEFL 122
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Qy 60 GRUPLDLAQRGHQDIVRYL 79
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |

RESULT 11
ENTRY S18188 #type complete
TITLE notch protein homolog - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
13-Aug-1999
ACCESSIONS S18188
REFERENCE S18188
#authors Weinmaster, G.; Roberts, V.J.; Lemke, G.
#journal Development (1991) 113:199-205
#title A homolog of Drosophila Notch expressed during mammalian
development.
#cross-references MUID:92111383
#accession S18188
#molecule_type mRNA
#residues 1-2531 #label WEI
#cross-references EMBL:X57405; NID:g57634; PID:g57635
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology

```

```

FEATURE
987-1018      #domain EGF homology #label EGF1\
1025-1056      #domain EGF homology #label EGF\
1233-1264      #domain EGF homology #label EGF2\
1917-1949      #domain ankyrin repeat homology #label AN1\
1950-1982      #domain ankyrin repeat homology #label AN2\
1984-2016      #domain ankyrin repeat homology #label AN3\
2017-2049      #domain ankyrin repeat homology #label AN4\
2050-2082      #domain ankyrin repeat homology #label AN5\
SUMMARY
Query Match      17.58; Score 156; DB 2; Length 2531;
Best Local Similarity 42.98; Pred.No. 2.58e-11;
Matches 33; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Db 2028 VNNVDAAVLLKNGANKDMQNNKE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2086
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 3  MGNVHVAALLNNGADSNCEDPFTFSRPVHDAAREGFLDTLVVLHSGSARLDYRDAGRL 62
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 2087 PRDIAQERMHHDIVRL 2103
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 PLDLAQERGHQDIVRYL 79

RESULT 12
ENTRY
TITLE      A40043      #type complete
ORGANISM    notch protein homolog TAN-1 precursor - human
DATE        21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change
13-Aug-1999
ACCESSIONS  A40043
REFERENCE    Ellis, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds,
T.C.; Smith, S.D.; Sklar, J.
Cell (1991) 66:649-661
#journal     Cell (1991) 66:649-661
#title       TAN-1, the human homolog of the Drosophila Notch gene, is
broken by chromosomal translocations in T lymphoblastic
neoplasms.
#cross-references MUID:91347367
#accession    A40043
#status       preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
#molecule_type mRNA
#residues     1-2555 #label ELL
#cross-references GB:M73980
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
FEATURE
261-292      #domain EGF homology #label EGF1\
494-525      #domain EGF homology #label EGF1\
987-1018      #domain EGF homology #label EGF2\
1149-1180      #domain EGF homology #label EGF2\
1187-1218      #domain EGF homology #label EGF3\
1233-1264      #domain EGF homology #label EGF3\
1927-1959      #domain ankyrin repeat homology #label AN1\
1960-1992      #domain ankyrin repeat homology #label AN2\
1994-2026      #domain ankyrin repeat homology #label AN3\
2027-2059      #domain ankyrin repeat homology #label AN4\
2060-2092      #domain ankyrin repeat homology #label AN5\
SUMMARY
Query Match      17.38; Score 154; DB 2; Length 2555;
Best Local Similarity 42.98; Pred.No. 5.86e-11;
Matches 33; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Db 2038 VNNVDAAVLLKNGANKDMQNNKE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2096
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 3  MGNVHVAALLNNGADSNCEDPFTFSRPVHDAAREGFLDTLVVLHSGSARLDYRDAGRL 62
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 2097 PRDIAQERMHHDIVRL 2113
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QY 63 PLDLAQERGHQDIVRYL 79

```

```

RESULT 13
ENTRY
TITLE      A46019      #type complete
ALTERNATE_NAMES Notch-1 protein - mouse
ORGANISM    Notch protein
DATE        #formal_name Mus musculus #common_name house mouse
22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
20-Sep-1999
ACCESSIONS  A46019; S25144
REFERENCE    A46019
del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins,
N.A.; Copeland, N.G.; Gridley, T.
Genomics (1993) 15:259-264
#journal     Genomics (1993) 15:259-264
#title       Cloning, analysis, and chromosomal localization of Notch-1, a
mouse homolog of Drosophila Notch.
#cross-references MUID:93194170
#accession    A46019
#status       not compared with conceptual translation
#molecule_type nucleic acid
#residues     1-2531 #label DEL
#cross-references GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
PID:g288503
#note        sequence extracted from NCBI backbone (NCBIP:127318)
REFERENCE    S25144
Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.;
Gendron-Maguire, M.; Greenspan, R.J.; McMahon, A.P.;
Gridley, T.
#journal     submitted to the EMBL Data Library, April 1992
#description Expression pattern of Notch, a mouse homolog of Drosophila
Notch, suggests an important role in early postimplantation
mouse development.
#accession    S25144
#molecule_type mRNA
#residues     1551-2108, 'Q', '2110-2114, 'ALP', 2118-2170 #label FRA
#cross-references EMBL:Z11886
GENETICS
#gene         notch-1
#map_position 2
#note         proximal region of chromosome 2
#superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
CLASSIFICATION
FEATURE
106-138      #domain EGF homology #label EGF1\
144-175      #domain EGF homology #label EGF1\
222-254      #domain EGF homology #label EGF2\
261-292      #domain EGF homology #label EGF2\
339-370      #domain EGF homology #label EGF3\
416-449      #domain EGF homology #label EGF3\
456-487      #domain EGF homology #label EGF3\
494-525      #domain EGF homology #label EGF5\
532-563      #domain EGF homology #label EGF6\
607-638      #domain EGF homology #label EGF7\
682-713      #domain EGF homology #label EGF8\
757-788      #domain EGF homology #label EGF8\
795-826      #domain EGF homology #label EGF10\
873-904      #domain EGF homology #label EGF11\
911-942      #domain EGF homology #label EGF12\
949-980      #domain EGF homology #label EGF13\
987-1018      #domain EGF homology #label EGF14\
1025-1056      #domain EGF homology #label EGF15\
1063-1094      #domain EGF homology #label EGF16\
1149-1180      #domain EGF homology #label EGF17\
1187-1218      #domain EGF homology #label EGF18\
1233-1264      #domain EGF homology #label EGF4\
1352-1383      #domain EGF homology #label EGF4\
1391-1425      #domain ankyrin repeat homology #label AN1\
1917-1948      #domain ankyrin repeat homology #label AN2\
1949-1981      #domain ankyrin repeat homology #label AN3\
1983-2015      #domain ankyrin repeat homology #label AN4\
2016-2048      #domain ankyrin repeat homology #label AN5\
2049-2081      #domain ankyrin repeat homology #label AN5\
SUMMARY
#length 2531 #molecular-weight 271312 #checksum 6611

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Query Match      16.78; Score 149; DB 2; Length 2531;
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Matches 29; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

Db 2027 VNNYDAAVLLKNGKANDIENKEETSLFSLIRRESYETAKVLLDHFANR-DITDHMDRL 2085
QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVYRDAGRL 62

Db 2086 PRDIAQRMHHDIVRL 2102
QY 63 PLDLAQERGHQDIVRYL 79

RESULT 14
ENTRY      A56695      #type fragment
TITLE      notch2 protein homolog - human (fragment)
ALTERNATE_NAMES notch hn
ORGANISM   Homo sapiens #common_name man
DATE       21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change
ACCESSIONS A56695; G02458
REFERENCE   Stifani, S.; Blaumueller, C.M.; Redhead, N.J.; Hill, R.E.;
            Artavanis-Tsakonas, S.
#journal    Nature Genet. (1992) 2:119-127
#title      Human homologs of a Drosophila enhancer of split gene product
            Define a novel family of nuclear proteins.
#cross-references MUID:93265135
#accession  A56695
#status     preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues   1-638 #label STI
#cross-references GB:M99437; NID:g189263; PIDN:AAA36377.1; PID:g189264
            H01314
#authors    Fisher, E.M.C.
#submission submitted to the EMBL Data Library, March 1996
#accession  G02458
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   157-221 #label FIS
#cross-references EMBL:U50549; NID:g1293642; PIDN:AAB17664.1;
            PID:g1293643
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
            repeat homology; EGF homology
            tandem repeat; transmembrane protein
KEYWORDS
FEATURE
69-101      #domain ankyrin repeat homology #label AN1\
102-134      #domain ankyrin repeat homology #label AN2\
136-168      #domain ankyrin repeat homology #label AN3\
169-201      #domain ankyrin repeat homology #label AN4\
202-234      #domain ankyrin repeat homology #label AN5\
SUMMARY      #length 638 #checksum 7438

Query Match      16.68; Score 148; DB 2; Length 638;
Best Local Similarity 39.08; Pred. No. 6.67e-10;
Matches 30; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

Db 180 VNNYEATLLKNGANRDMQDNKE-ETPLFLAAREGSYEAAKILLDHFANRDTDHMDRL 238
QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVYRDAGRL 62

Db 239 PRDVARDRMHHDIVRL 255
QY 63 PLDLAQERGHQDIVRYL 79

RESULT 15
ENTRY      A49128      #type complete
TITLE      cell-fate determining gene Notch2 protein - rat
ORGANISM   Rattus norvegicus #common_name Norway rat
DATE       21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
            13-Aug-1999
ACCESSIONS A49128
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REFERENCE A49128
Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development (1992) 116:931-941
#journal
#title      Notch2: a second mammalian Notch gene.
#cross-references MUID:93202015
#accession  A49128
#status     preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues   1-2471 #label WEI
#experimental_source Schwann cell
#note       #sequence extracted from NCBI backbone (NCBIP:127811)
            #superfamily unassigned ankyrin repeat proteins; ankyrin
            repeat homology; EGF homology
CLASSIFICATION
FEATURE
264-295      #domain EGF homology #label EGX1\
799-830      #domain EGF homology #label EGX1\
877-908      #domain EGF homology #label EGX2\
1029-1060     #domain EGF homology #label EGX\
1067-1098     #domain EGF homology #label EGX3\
1153-1184     #domain EGF homology #label EGX3\
1191-1222     #domain EGF homology #label EGX4\
1876-1908     #domain ankyrin repeat homology #label AN1\
1909-1941     #domain ankyrin repeat homology #label AN2\
1943-1975     #domain ankyrin repeat homology #label AN3\
1376-2008     #domain ankyrin repeat homology #label AN4\
2009-2041     #domain ankyrin repeat homology #label AN5\
SUMMARY      #length 2471 #molecular-weight 265367 #checksum 5929

Query Match      16.6%; Score 148; DB 2; Length 2471;
Best Local Similarity 39.0%; Pred. No. 6.67e-10;
Matches 30; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

Db 1987 VNNYEATLLKNGANRDMQDNKE-ETPLFLAAREGSYEAAKILLDHFANRDTDHMDRL 2045
QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVYRDAGRL 62

Db 2046 PRDVARDRMHHDIVRL 2062
QY 63 PLDLAQERGHQDIVRYL 79

Search completed: Thu Jul 20 08:42:09 2000
JOB time : 13 secs.
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FT VARSPLIC 1 42 MISSING (IN SHORT ISOFORM).  
SQ SEQUENCE 167 AA; 17870 MW; 88C4588A105ECB8F CRC64;

Query Match 100.0%; Score 892; DB 1; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.00e-191;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 MMGNVHVAALLNTGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLVDWDWG 102  
|||||  
QY 1 MMGNVHVAALLNTGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLVDWDWG 60  
|||||

Db 103 RLPLDLAQRGHODIVYRLRSAGCSLCSAGWSLCTAGNVAOTDGHFSFSSPRALELRGQ 162  
|||||  
QY 61 RLPLDLAQRGHODIVYRLRSAGCSLCSAGWSLCTAGNVAOTDGHFSFSSPRALELRGQ 120  
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Db 163 SQEQS 167  
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QY 121 SQEQS 125

RESULT 2  
ID CDN2 HUMAN STANDARD; PRT; 156 AA.  
AC P42771; Q15191;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)  
DE (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).  
GN CDKN2A OR CDKN2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94081956.  
RA Serrano M., Hannon G.J., Beach D.;  
RT "A new regulatory motif in cell-cycle control causing specific  
inhibition of cyclin D/CDK4.";  
RL Nature 366:704-707(1993).  
RN [2]  
RP SEQUENCE OF 51-152 FROM N.A.  
RX MEDLINE; 94204645.  
RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,  
RA Skolnick M.H.;  
RT "A cell cycle regulator potentially involved in genesis of many tumor  
types.";  
RL Science 264:436-440(1994).  
RN [3]  
RP SEQUENCE OF 1-20 FROM N.A.  
RX MEDLINE; 96182088.  
RA Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;  
RT "Regulation of p16CDKN2 expression and its implications for cell  
immortalization and senescence.";  
RL Mol. Cell. Biol. 16:859-867(1996).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.  
RX MEDLINE; 98421670.  
RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;  
RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6  
by the tumour suppressor p16INK4a.";  
RL Nature 395:237-243(1998).  
RN [5]  
RP REVIEW ON MELANOMA VARIANTS.  
RX MEDLINE; 96377761.  
RA Dracopoli N.C., Fountain J.W.;  
RT "CDKN2 mutations in melanoma.";  
RL Cancer Surv. 26:115-132(1996).  
RN [6]  
RP REVIEW ON VARIANTS.  
RX MEDLINE; 96303699.  
RA Smith-Soerensen B., Hovig E.;  
RT "CDKN2A (p16INK4A) somatic and germline mutations.";

Hum. Mutat. 7:294-303(1996).  
[7]  
RN VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
RX MEDLINE; 94338359.  
RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
(cyclin-dependent kinase-4 inhibitor) gene in human primary non-small  
cell lung carcinomas.";  
RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
RN [8]  
RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-136 & THR-148.  
RX MEDLINE; 95078916.  
RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,  
RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
RT "Germline p16 mutations in familial melanoma.";  
RL Nat. Genet. 8:15-21(1994).  
RN [9]  
RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
RX MEDLINE; 95060835.  
RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
RA Abraham J.M., Meltzer S.J.;  
RT "The MTS1 gene is frequently mutated in primary human esophageal  
tumors.";  
RL Oncogene 9:3737-3741(1994).  
RN [10]  
RP VARIANTS.  
RX MEDLINE; 95188190.  
RA Okamoto A., Hussian S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,  
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;  
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
primary and metastatic lung cancer.";  
RL Cancer Res. 55:1448-1451(1995).  
RN [11]  
RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
RX MEDLINE; 96121580.  
RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,  
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
kindreds.";  
RL Hum. Mol. Genet. 4:1845-1852(1995).  
RN [12]  
RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.  
RX MEDLINE; 95375774.  
RA Ranade K., Hussussian C.J., Sikorski R.S., Varnus H.E.,  
RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
RA Dracopoli N.C.;  
RT "Mutations associated with familial melanoma impair p16INK4  
function.";  
RL Nat. Genet. 10:114-116(1995).  
RN [13]  
RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.  
RX MEDLINE; 96323259.  
RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,  
RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
RA Tselbacher K.J., Sober A.J., Haber D.A.;  
RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
familial melanoma: analysis of a clinic-based population.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
RN [14]  
RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
RX MEDLINE; 97472457.  
RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,  
RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,  
RA Bishop D.T., Bishop J.N.;  
RT "Germline mutations of the CDKN2 gene in UK melanoma families.";  
RL Hum. Mol. Genet. 6:2061-2067(1997).  
RN [15]  
RP VARIANTS FAMILIAL MELANOMA.  
RX MEDLINE; 98087572.  
RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,  
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone

	families in France.";	
RT	Hum. Mol. Genet. 7:209-216(1998).	
RL	[16]	
RN	ERRATUM.	
RA	Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,	
RP	Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-Delabarere B.;	
RR	Hum. Mol. Genet. 7:941-941(1998).	
RN	[17]	
RV	VARIANT PANCREATIC CARCINOMA CYS-146.	
RA	Moskaluk C.A., Hruban R.H., Lietman A., Smrk T., Fusaro L.,	
RA	Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;	
RA	"Novel germline p16INK4 allele (Aspl45cys) in a family with multiple	
RT	pancreatic carcinomas."	
RT	Hum. Mutat. 12:70-70(1998).	
RL	[18]	
RN	VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.	
RA	Gretarsdottir S., Olafsdottir G.H., Borg A.;	
RP	"Five novel somatic CDKN2/p16 mutations identified in melanoma,	
RT	glioma and carcinoma of the pancreas".	
RT	Hum. Mutat. 12:212-212(1998).	
CC	-I- FUNCTION TO INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS	
CC	ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE	
CC	REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.	
CC	-I- SUBUNIT: HETERODIMERS WITH CDK4 OR CDK6.	
CC	-I- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A	
CC	WIDE RANGE OF TISSUES.	
CC	-I- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE	
CC	INHIBITORS.	
CC	-I- SIMILARITY: CONTAINS 4 ANK REPEATS.	
CC	-----	
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CC	-----	
EMBL:	L27211; AAA92554.1; --	
DR	EMBL; U12820; AAB60645.1; --	
DR	EMBL; U12818; AAB60645.1; JOINED.	
DR	EMBL; U12819; AAB60645.1; JOINED.	
DR	EMBL; S69804; AAID4048.1; --	
DR	EMBL; X94154; CAAG3870.1; --	
DR	PDB; 1BI7; 16-FEB-99.	
DR	MDM; 600160; --	
DR	PFAM; PF00023; ank; 3.	
KW	Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;	
KW	Polymorphism; 3D-structure.	
FT	DOMAIN 12 141	4 X ANK MOTIF REPEATS.
FT	REPEAT 12 43	X ANK MOTIF 1 (INCOMPLETE).
FT	REPEAT 44 75	ANK MOTIF 2.
FT	REPEAT 77 109	ANK MOTIF 3.
FT	REPEAT 110 141	ANK MOTIF 4.
FT	VARIANT 14 14	D -> E (IN A BILIARY TRACT TUMOR). /FTid=VAR_001408.
FT	VARIANT 16 16	L -> P (IN A BILIARY TRACT TUMOR AND A FAMILIAL MELANOMA). /FTid=VAR_001409.
FT	VARIANT 20 20	A -> P (IN A LONG TUMOR AND MELANOMA). /FTid=VAR_001410.
FT	VARIANT 20 20	A -> S (IN A BILIARY TRACT TUMOR). /FTid=VAR_001411.
FT	VARIANT 23 23	G -> D (IN A PANCREAS TUMOR). /FTid=VAR_001412.
FT	VARIANT 24 24	R -> C (IN MELANOMA). /FTid=VAR_001413.
FT	VARIANT 24 24	R -> P (IN FAMILIAL MELANOMA AND MELANOMA). /FTid=VAR_001414.
FT	VARIANT 26 26	E -> D (IN A BILIARY TRACT TUMOR). /FTid=VAR_001415.
FT	VARIANT 32 32	L -> P (IN FAMILIAL MELANO)

[illegible]



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CC EMBL; U17075; AAC50075.1; -  
DR EMBL; L36844; AAA50282.1; -  
DR EMBL; S69805; AAD14049.1; -  
CC MIM; 600431; -  
CC Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.  
KW DOMAIN 13 103  
FT REPEAT 13 39  
FT REPEAT 13 39  
FT REPEAT 13 39  
FT VARIANT 47 47  
FT VARIANT 47 47  
FT VARIANT 50 50  
FT VARIANT 50 50  
FT CONFLICT 20 21  
FT CONFLICT 23 23  
FT CONFLICT 32 34  
FT CONFLICT 32 34  
SQ SEQUENCE 138 AA; 14722 MW; 0D6FFBDA6FEAD21 CRC64;

Query Match 52.9%; Score 472; DB 1; Length 139;  
Best Local Similarity 74.4%; Pred. No. 6.14e-86;  
Matches 61; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Db 54 MMGSAQVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVLRHAGARLDVCDANG 113  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVLRHAGARLDVCDANG 60  
Db 114 RLPVDAEERGHQDIYVYLRSA 135  
QY 61 RLPDLAQERGHQDIYVYLRSA 82

RESULT 4  
ID CDN5\_MOUSE STANDARD; PRT; 130 AA.  
AC P55271;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).  
GN CDKN2B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95380169.  
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;  
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes";  
RL Oncogene 11:635-645(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J X DBA;  
RX MEDLINE; 97322242.  
RA Malumbres M., de Castro I., Santos J., Melendez B., Manques R.,  
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by  
RT deletion and de novo methylation with independence of p16INK4a  
RT alterations in murine primary T-cell lymphomas";  
RL Oncogene 14:1361-1370(1997).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
CC INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN  
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL  
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.

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DR EMBL; U66085; AAB39833.1; -  
DR EMBL; U66084; AAB39833.1; JOINED.  
DR MGD; MGI:104737; CDKN2B.  
DR PFAM; PF00023; ank; 3.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.  
FT DOMAIN 5 95  
FT REPEAT 5 31  
FT REPEAT 65 95  
FT REPEAT 65 95  
SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 51.7%; Score 461; DB 1; Length 130;  
Best Local Similarity 73.2%; Pred. No. 3.05e-83;  
Matches 60; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 46 MMGSAQVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVLRHAGARLDVCDANG 105  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVLRHAGARLDVCDANG 60  
Db 106 RLPVDAEERGHQDIYVYLRSA 127  
QY 61 RLPDLAQERGHQDIYVYLRSA 82

RESULT 5  
ID CDN5\_RAT STANDARD; PRT; 130 AA.  
AC P55272;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).  
GN CDKN2B OR INK4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96001392.  
RA Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,  
RA Tsuchiya H., Kikuchi Y., Mitani H.;  
RT "Molecular genetic basis of renal carcinogenesis in the Eker rat  
RT model of tubular sclerosis (tsc2).";  
RL Mol. Carcinog. 14:23-27(1995).  
RN [2]  
RP SEQUENCE OF 46-86 FROM N.A.  
RX MEDLINE; 95228036.  
RA Knapik D.F., Serrano M., Beach D., Trono D., Walker C.L.;  
RT "Association of rat p15INK4B/p16INK4 deletions with tumorigenesis 5 in  
RT kidney epithelial cell lines but not primary renal tumors";  
RL Cancer Res. 55:1607-1612(1995).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
CC INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN  
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL  
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.

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DR EMBL: S79760; AAB35360.1; -;  
DR EMBL: S77734; CAB33639.1; -;  
DR PFAM: PF00023; ank; 3.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,  
FT CHAIN 1 130 LONG FORM.  
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,  
FT CHAIN 46 130 SHORT FORM.  
FT INIT\_MET 46 46 FOR THE SHORT FORM.  
FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.  
FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).  
FT REPEAT 65 95 ANK MOTIF 2.  
SQ SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match 51.28; Score 457; DB 1; Length 130;  
Best Local Similarity 72.08; Pred. No. 2.90e-82;  
Matches 59; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

Db 46 MMGSAQVAELLHAGPNCAPALTRPVHDAAREGFLDTLMLHKGARLDVCDWG 105  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVVLHSGARLDVCDWG 60  
Db 106 RLPVDAEQQHDIARYLHAA 127  
QY 61 RLPDLAQERGHQDIVRYLRS 82

RESULT 6  
ID CDN2\_MONDO STANDARD; PRT; 171 AA.  
AC Q77617;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4)  
DE (TUMOR SUPPRESSOR CDKN2A).  
GN CDKN2A.

OS Monodelphis domestica (Short-tailed grey opossum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Metatheria; Didelphimorphia; Didelphidae; Monodelphis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherburn T.E., Gale J.M., Lev R.D.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR  
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
CC INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.

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DR EMBL: AF064808; AAC23669.1; -;  
DR EMBL: AF064808; AAC23670.1; -;  
DR PFAM: PF00023; ank; 3.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT DOMAIN 46 169 4 X ANK MOTIF REPEATS.  
FT REPEAT 46 77 ANK MOTIF 1 (INCOMPLETE).

FT REPEAT 78 109 ANK MOTIF 2.  
FT REPEAT 111 143 ANK MOTIF 3.  
FT REPEAT 144 169 ANK MOTIF 4.  
FT VARSPLIC 1 34 MISSING (IN SHORT ISOFORM).  
SQ SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;

Query Match 48.78; Score 434; DB 1; Length 171;  
Best Local Similarity 71.38; Pred. No. 1.19e-76;  
Matches 57; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

Db 86 MMGNVRLAAILLOYGAENPTDPTTLTPVHDAAREGFLDTLMLHKGARLDVCDWG 145  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVVLHSGARLDVCDWG 60  
Db 146 RLPVDAEQQHHLVYVYLR 165  
QY 61 RLPDLAQERGHQDIVRYLRS 80

RESULT 7  
ID CDN7\_HUMAN STANDARD; PRT; 166 AA.  
AC P55273; Q13102;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).  
GN CDKN2D.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=NONE MARROW;  
RX MEDLINE; 96121373.  
RA Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,  
RA Lahti J.M., Sherr C.J., Downing J.R.;  
RT "Molecular cloning, expression pattern, and chromosomal localization  
RT of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases."  
RL Genomics 29:632-630(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96362662.  
RA Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,  
RA Zariwala M., Matera A.G., Xiong Y.;  
RT "Isolation and characterization of p19INK4d, a p16-related inhibitor  
RT specific to CDK6 and CDK4."  
RL Mol. Biol. Cell 7:57-70(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95257949.  
RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;  
RT "Identification of human and mouse p19, a novel CDK4 and CDK6  
RT inhibitor with homology to p16ink4."  
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RN [4]  
RP SEQUENCE FROM N.A.  
RA Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,  
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RN [5]  
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RT by the tumour suppressor p16INK4a."  
RL Nature 395:237-243(1998).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RX MEDLINE; 98455510.  
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GN NOTCH1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE-SCHWANN CELL;  
RX MEDLINE; 9211383.  
RA Weinmaster G.; Roberts V.J.; Lenke G.;  
RT "A homolog of Drosophila Notch expressed during mammalian  
development.";  
RL Development 113:199-205(1991).  
RN (2)  
RP REVISIONS TO 1652-1653.  
RA Weinmaster G.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: REQUIRED FOR THE CORRECT DIFFERENTIATION OF A NUMBER  
OF TISSUES.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST LEVELS OCCUR BETWEEN  
DAYS 12 AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE  
ADULT.  
CC -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.  
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
DR EMBL; X57405; CAA40667.1; -;  
DR HSP; P00740; LIXA.  
DR PRINTS; PR00010; EGFBL00D.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 22.  
DR PROSITE; PS00022; EGF\_1; 35.  
DR PROSITE; PS01186; EGF\_2; 26.  
DR PROSITE; PS01187; EGF\_CA; 21.  
DR PFAM; PF00008; EGF; 36.  
DR PFAM; PF00023; ank; 6.  
DR PFAM; PF00066; notch; 3.  
DR KW Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain;  
KW Transmembrane; Signal; Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 2531 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.  
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FT TRANSMEM 1724 1746 POTENTIAL.  
FT DOMAIN 1747 2531 CYTOPLASMIC (POTENTIAL).  
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FT DOMAIN 140 176 EGF-LIKE 4.  
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FT DOMAIN 218 255 EGF-LIKE 6.  
FT DOMAIN 257 293 EGF-LIKE 7.  
FT DOMAIN 295 333 EGF-LIKE 8.  
FT DOMAIN 335 371 EGF-LIKE 9.  
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FT DOMAIN 412 450 EGF-LIKE 11.  
FT DOMAIN 452 488 EGF-LIKE 12.  
FT DOMAIN 490 526 EGF-LIKE 13.  
FT DOMAIN 528 564 EGF-LIKE 14.  
FT DOMAIN 566 601 EGF-LIKE 15.  
FT DOMAIN 603 639 EGF-LIKE 16.  
FT DOMAIN 641 676 EGF-LIKE 17.  
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FT DOMAIN 791 827 EGF-LIKE 21, CALCULON-BINDING (POTENTIAL).  
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233 243 BY SIMILARITY.  
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243 254 BY SIMILARITY.  
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254 272 BY SIMILARITY.  
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272 281 BY SIMILARITY.  
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387 398 BY SIMILARITY.  
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398 409 BY SIMILARITY.  
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409 429 BY SIMILARITY.  
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429 438 BY SIMILARITY.  
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438 449 BY SIMILARITY.  
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467 476 BY SIMILARITY.  
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487 505 BY SIMILARITY.  
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505 514 BY SIMILARITY.  
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514 525 BY SIMILARITY.  
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525 543 BY SIMILARITY.  
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543 552 BY SIMILARITY.  
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552 554 BY SIMILARITY.  
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563 570 BY SIMILARITY.  
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FT DISULFID 575 589 BY SIMILARITY.  
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FT DISULFID 607 618 BY SIMILARITY.  
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FT DISULFID 645 655 BY SIMILARITY.  
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FT DISULFID 682 693 BY SIMILARITY.  
FT DISULFID 687 702 BY SIMILARITY.  
FT DISULFID 704 713 BY SIMILARITY.  
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FT DISULFID 725 739 BY SIMILARITY.  
FT DISULFID 741 750 BY SIMILARITY.  
FT DISULFID 757 768 BY SIMILARITY.  
FT DISULFID 762 777 BY SIMILARITY.  
FT DISULFID 779 788 BY SIMILARITY.  
FT DISULFID 795 806 BY SIMILARITY.  
FT DISULFID 800 815 BY SIMILARITY.  
FT DISULFID 817 826 BY SIMILARITY.  
FT DISULFID 833 844 BY SIMILARITY.  
FT DISULFID 838 855 BY SIMILARITY.  
FT DISULFID 857 867 BY SIMILARITY.  
FT DISULFID 874 885 BY SIMILARITY.  
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FT DISULFID 896 905 BY SIMILARITY.  
FT DISULFID 912 923 BY SIMILARITY.  
FT DISULFID 923 932 BY SIMILARITY.  
FT DISULFID 934 943 BY SIMILARITY.  
FT DISULFID 988 999 BY SIMILARITY.  
FT DISULFID 993 1008 BY SIMILARITY.  
FT DISULFID 1010 1019 BY SIMILARITY.  
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FT DISULFID 1150 1161 BY SIMILARITY.  
FT DISULFID 1155 1170 BY SIMILARITY.  
FT DISULFID 1172 1181 BY SIMILARITY.  
FT DISULFID 1188 1199 BY SIMILARITY.  
FT DISULFID 1193 1208 BY SIMILARITY.

...  
Note: remainder of annotations omitted.

Query Match 17.3%; Score 154; DB 1; Length 2444;

Best Local Similarity 42.9%; Pred. No. 1.06e-12;

Matches 33; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Db 2039 VNNVDAVLLKNGANKMONNRE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2097

QY 3 MGNVHVAALLNTGADSNCEPTTFSPRHDAAAREGLDFLVVLHGSGARLVDWAGRL 62

Db 2098 PRDIAQERHHDIVRL 2114

QY 63 PLDLAQERGHQDIVRYL 79

RESULT 13

ID NTC1\_MOUSE STANDARD; PRT; 2531 AA.

AC 001705;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (NOTCH PROTEIN).

GN NOTCH1 OR NOTCH.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Mus.









## EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN	1161	1204	EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).	FT DISULFID	799	808	BY SIMILARITY.
FT DOMAIN	1206	1245	EGF-LIKE 31.	FT DISULFID	815	827	BY SIMILARITY.
FT DOMAIN	1247	1288	EGF-LIKE 32.	FT DISULFID	821	836	BY SIMILARITY.
FT DOMAIN	1290	1326	EGF-LIKE 33.	FT DISULFID	838	847	BY SIMILARITY.
FT DOMAIN	1336	1374	EGF-LIKE 34.	FT DISULFID	854	865	BY SIMILARITY.
FT REPEAT	1388	1428	LIN/NOTCH 1.	FT DISULFID	859	874	BY SIMILARITY.
FT REPEAT	1429	1467	LIN/NOTCH 2.	FT DISULFID	876	885	BY SIMILARITY.
FT REPEAT	1468	1503	LIN/NOTCH 3.	FT DISULFID	892	902	BY SIMILARITY.
FT REPEAT	1784	1816	CDC10/SWI6 1.	FT DISULFID	897	911	BY SIMILARITY.
FT REPEAT	1817	1865	CDC10/SWI6 2.	FT DISULFID	913	922	BY SIMILARITY.
FT REPEAT	1866	1898	CDC10/SWI6 3.	FT DISULFID	929	940	BY SIMILARITY.
FT REPEAT	1899	1932	CDC10/SWI6 4.	FT DISULFID	934	949	BY SIMILARITY.
FT REPEAT	1933	1965	CDC10/SWI6 5.	FT DISULFID	951	960	BY SIMILARITY.
FT REPEAT	1966	1998	CDC10/SWI6 6.	FT DISULFID	967	978	BY SIMILARITY.
FT DISULFID	43	55	BY SIMILARITY.	FT DISULFID	972	987	BY SIMILARITY.
FT DISULFID	49	66	BY SIMILARITY.	FT DISULFID	989	998	BY SIMILARITY.
FT DISULFID	68	77	BY SIMILARITY.	FT DISULFID	1005	1016	BY SIMILARITY.
FT DISULFID	83	94	BY SIMILARITY.	FT DISULFID	1010	1023	BY SIMILARITY.
FT DISULFID	88	107	BY SIMILARITY.	FT DISULFID	1025	1034	BY SIMILARITY.
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FT DISULFID	163	175	BY SIMILARITY.	FT DISULFID	1094	1109	BY SIMILARITY.
FT DISULFID	169	184	BY SIMILARITY.	FT DISULFID	1111	1120	BY SIMILARITY.
FT DISULFID	186	195	BY SIMILARITY.	FT DISULFID	1127	1138	BY SIMILARITY.
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FT DISULFID	245	261	BY SIMILARITY.	FT DISULFID	1194	1203	BY SIMILARITY.
FT DISULFID	263	272	BY SIMILARITY.	FT DISULFID	1210	1223	BY SIMILARITY.
FT DISULFID	279	292	BY SIMILARITY.	FT DISULFID	1215	1233	BY SIMILARITY.
FT DISULFID	286	301	BY SIMILARITY.	FT DISULFID	1235	1244	BY SIMILARITY.
FT DISULFID	303	312	BY SIMILARITY.	FT DISULFID	1251	1262	BY SIMILARITY.
FT DISULFID	319	330	BY SIMILARITY.	FT DISULFID	1256	1276	BY SIMILARITY.
FT DISULFID	324	339	BY SIMILARITY.	FT DISULFID	1278	1287	BY SIMILARITY.
FT DISULFID	341	350	BY SIMILARITY.	FT DISULFID	1294	1305	BY SIMILARITY.
FT DISULFID	356	367	BY SIMILARITY.	FT DISULFID	1299	1314	BY SIMILARITY.
FT DISULFID	361	378	BY SIMILARITY.	FT DISULFID	1316	1325	BY SIMILARITY.
FT DISULFID	380	389	BY SIMILARITY.	FT DISULFID	1340	1351	BY SIMILARITY.
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FT DISULFID	403	418	BY SIMILARITY.				
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FT DISULFID	479	494	BY SIMILARITY.				
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FT DISULFID	512	523	BY SIMILARITY.				
FT DISULFID	517	532	BY SIMILARITY.				
FT DISULFID	534	543	BY SIMILARITY.				
FT DISULFID	550	560	BY SIMILARITY.				
FT DISULFID	553	569	BY SIMILARITY.				
FT DISULFID	571	580	BY SIMILARITY.				
FT DISULFID	587	598	BY SIMILARITY.				
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FT DISULFID	646	655	BY SIMILARITY.				
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FT DISULFID	667	682	BY SIMILARITY.				
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FT DISULFID	721	730	BY SIMILARITY.				
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FT DISULFID	744	759	BY SIMILARITY.				
FT DISULFID	761	770	BY SIMILARITY.				
FT DISULFID	776	787	BY SIMILARITY.				
FT DISULFID	781	797	BY SIMILARITY.				

Note: remainder of annotations omitted.

Query Match 16.5%; Score 147; DB 1; Length 2318;

Best Local Similarity 40.3%; Pred. No. 2.53e-11;

Matches 31; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

Db 1950 VNNVEATLALKNGANKMDSKE-ETPLFLAAREGSYEAKLLLDHLANREITDHLRL 2008

QY 3 MGNVHVAALLNTYGADSNCEPTTFSRPVHDAREGFDTLVVLHGSGARLDYRDWGR 62

Db 2009 PRDVAQERHQDIVRL 2025

QY 63 PLDAQERHQDIVRYL 79

RESULT 15

ID NOTC\_BRARE STANDARD; PRT; 2437 AA.

AC P46530;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN PRECURSOR.

GN NOTCH.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

OC Cyprinoidae; Cyprinidae; Rasbora; Danio.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=EMBRYO;







\*\*\*\*\*  
MPSRELH  
\*\*\*\*\*  
(TM)  
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MParch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:42:52 2000; MasPar time 16.56 Seconds  
523.462 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-016-869A-6  
Description: (1-125) from US09016869A.pep  
Perfect Score: 892  
Sequence: 1 MMGNVHVALLNYGADSN.....SFSSSTPRALRQGSQEQS 125

Scoring table: PAM 150  
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sprembl12  
1:sp-archaea 2:sp-bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp-organelle  
9:sp-phage 10:sp\_plant 11:sp-rodent 12:sp\_unclassified  
13:sp-vertebrate 14:sp\_virus

Statistics: Mean 41.331; Variance 69.208; scale 0.597

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description	Pred. No.
1	892	100.0	168	11	P97510 CYCLIN DEPENDENT KINAS	1.74e-185
2	890	99.8	168	11	O89088 CYCLIN DEPENDENT KINAS	5.44e-185
3	806	90.4	113	11	O921C2 CYCLIN-DEPENDENT KINAS	3.20e-164
4	492	55.2	102	6	O9XS51 P15/CDKN2A/MTS1 (FRAGM	7.62e-88
5	488	54.7	86	6	O9XS52 P15/MTS2/CDKN2B (FRAGM	6.86e-87
6	473	53.0	115	4	O16361 CELL CYCLE NEGATIVE RE	2.55e-83
7	461	51.7	86	11	O921C1 CYCLIN-DEPENDENT KINAS	1.80e-80
8	453	50.8	86	11	O54846 CYCLIN-DEPENDENT KINAS	1.42e-78
9	238	26.7	124	13	O9W618 P13CDKN2X.	2.15e-29
10	235	26.3	124	13	P70087 CDKN2X PROTEIN.	9.59e-29
11	214	24.0	58	6	O97886 CYCLIN-DEPENDENT KINAS	2.98e-24
12	163	18.3	835	4	O9Y2V6 HYPOTHETICAL 92.9 KD P	8.57e-14
13	160	17.9	251	11	O61905 NOTCH PROTEIN HOMOLOG	3.33e-13
14	156	17.5	1194	13	O9W737 NOTCH-1 (FRAGMENT).	2.01e-12
15	153	17.2	735	13	O93617 NOTCH HOMOLOGUE 2.	7.66e-12
16	152	17.0	2447	13	O13149 NOTCH 2 (FRAGMENT).	1.19e-11
17	148	16.6	389	11	O60941 NOTCH-2 (FRAGMENT).	6.99e-11
18	148	16.6	486	14	O96796 NOTCH2 (FRAGMENT).	6.99e-11
19	148	16.6	497	14	O96793 NOTCH2 (FRAGMENT).	6.99e-11
20	148	16.6	497	14	O96794 NOTCH2 (FRAGMENT).	6.99e-11

21	148	16.6	547	14	O96795 NOTCH2 (FRAGMENT).	6.99e-11
22	148	16.6	638	4	O04721 NEUROGENIC LOCUS NOTCH	6.99e-11
23	148	16.5	2470	11	O35516 CELL SURFACE PROTEIN.	1.08e-10
24	147	16.5	2321	4	O9Y6L8 NOTCH3.	1.08e-10
25	146	16.4	683	13	O93616 KITAA0379 (FRAGMENT).	4.02e-10
26	144	16.1	882	4	O15084 NOTCH HOMOLOG (FRAGMEN	5.21e-10
27	143	16.0	248	5	O44115 NOTCH HOMOLOG (FRAGMEN	5.37e-09
28	138	15.5	1476	13	O90285 NOTCH-3 HOMOLOG (FRAGM	8.23e-08
29	137	15.4	703	13	O93618 NOTCH HOMOLOGUE 3.	1.26e-08
30	136	15.2	1719	4	O13768 ALT. ANKYRIN (VARIANT	1.26e-08
31	136	15.2	1848	11	O61302 ANKYRIN 1, ERYTHROID (	1.26e-08
32	136	15.2	1856	4	O99407 ANKYRIN.	2.96e-08
33	134	15.0	854	11	O92261 SEX-DETERMINATION PROT	4.50e-08
34	133	14.9	1549	5	O24241 ANKYRIN.	1.04e-07
35	131	14.7	1411	5	O02989 ALPHA-LATROINSECTOTOXI	1.59e-07
36	130	14.6	1088	4	O13484 ANKYRIN G119.	2.41e-07
37	130	14.6	4377	4	O12955 ANKYRIN G.	2.41e-07
38	129	14.5	1786	5	O17344 UNC-44 (FRAGMENT).	2.41e-07
39	129	14.5	1809	5	O17487 E. ELEGANS ANKYRIN-REL	2.41e-07
40	129	14.5	1815	5	O17488 C. ELEGANS ANKYRIN-REL	2.41e-07
41	129	14.5	1867	5	O17486 C. ELEGANS ANKYRIN-REL	2.41e-07
42	129	14.5	2004	5	O61222 ZK1005.1 PROTEIN (FRAG	2.41e-07
43	129	14.5	2039	5	O17489 C. ELEGANS ANKYRIN-REL	2.41e-07
44	129	14.5	6994	5	O17343 UNC-44 ANKYRINS.	2.41e-07
45	127	14.2	1180	4	O92625 MYELOBLAST KIAA0229 (F	5.53e-07

ALIGNMENTS

RESULT	1					
ID	P97510	PRELIMINARY;	PRT;	168	AA.	
AC	P97510; P97937;					
DT	01-MAY-1997 (TREMBLrel. 03, Created)					
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)					
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)					
DE	CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR					
DE	PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4					
DE	(P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).					
GN	CDKN2A OR ELAPHA OR P16INK4A OR CDKN2A.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;					
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=DBA/2N; TISSUE=SPLEEN;					
RA	MEDLINE; 98151529.					
RA	ZHANG S., RAMSAY E.S., MOCK B.A.;					
RT	"cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and					
RT	p19ARF, is a candidate for the plasmacytoma susceptibility locus,					
RT	Pctrl.;"					
RL	Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).					
RN	[2]					
RP	SEQUENCE OF 1-42 FROM N.A.					
RC	STRAIN=VARIOUS STRAINS;					
RA	MEDLINE; 97179476.					
RA	HERZOG C.R., TOU M.;					
RT	"sequence variation and chromosomal mapping of the murine Cdkn2a tumor					
RT	suppressor gene.;"					
RL	Mamm. Genome 8:65-66(1997).					
RN	[3]					
RP	SEQUENCE OF 1-155 FROM N.A.					
RC	STRAIN=C57BL/6J X DBA;					
RA	MALOMBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES R.,					
RA	SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;					
RT	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.					
RN	[4]					
RP	SEQUENCE OF 1-42 FROM N.A.					
RC	STRAIN=DBA/2 AND C57BL/6;					
RA	MEDLINE; 95380169.					
RA	QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,					
RA	RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;					
RT	"Cloning and characterization of murine p16INK4a and p15INK4b genes.;"					
RL	Oncogene 11:635-645(1995).					

[5] SEQUENCE OF 1-42 FROM N.A.  
RP STRAIN-DBA/2 AND C57BL/6;  
RC GRESSANI K.M., ROLLINS L.A., MILLER M.S.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 1-11 FROM N.A.  
RC STRAIN-ICR SWISS;  
RX MEDLINE; 97128829.  
RA SOLOFF E.V., HERZOG C.R., YOU M.;  
RT "the 5'-flanking region of the E1 alpha form of the murine p16INK4a  
WT51 gene";  
RL Gene 180:213-215(1996).  
RN [7]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLF/EI AND MUS MUS MUSCULUS;  
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,  
RA PELLICER A., FERNANDEZ-PIQUERAS J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF04336; AAC08963.1; -;  
DR EMBL; AF04336; AAC08963.1; -;  
DR EMBL; U49280; AAC00052.1; -;  
DR EMBL; U66087; AAB39600.1; -;  
DR EMBL; U66086; AAB39600.1; JOINED.  
DR EMBL; AF004588; AAB61416.1; -;  
DR EMBL; U47018; AAC52987.1; -;  
DR EMBL; U79628; AAD00226.1; -;  
DR EMBL; U79625; AAD00223.1; -;  
DR EMBL; U79627; AAD00225.1; -;  
DR HSSP; P42771; 1BI7.  
DR MGD; MG1:104738; Cdkn2a.  
DR PFAM; PF00023; ank; 3.  
KW Kinase; Cyclin.  
SQ SEQUENCE 168 AA; 17941 MW; 89AD5E62 CRC32;  
  
Query Match 100.0%; Score 992; DB 11; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.74e-185;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 44 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAG 103  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAG 60  
|||||  
Db 104 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 163  
QY 61 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
|||||  
Db 164 SQEQS 168  
QY 121 SQEQS 125  
|||||  
  
RESULT 2 PRELIMINARY; PRT; 168 AA.  
ID O89088  
AC O89088;  
DT 01-NOV-1998 (TREMblrel. 08, Created)  
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR  
PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).  
GN CDKN2A OR E1ALPHA OR P16.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/CANPT; TISSUE-SPLEEN;  
RX MEDLINE; 98151529.  
RA ZHANG S., RAMSAY E.S., MOCK B.A.;  
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and  
p19ARF, is a candidate for the plasmacytoma susceptibility locus,  
Petr1.";

Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).  
RN [2]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN-MA/MAJ;  
RX MEDLINE; 97179476.  
RA HERZOG C.R., YOU M.;  
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor  
suppressor gene";  
RL Mamm. Genome 8:65-66(1997).  
RN [3]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;  
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,  
RA PELLICER A., FERNANDEZ-PIQUERAS J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF044335; AAC08962.1; -;  
DR EMBL; U49279; AAC00051.1; -;  
DR EMBL; U79626; AAD00224.1; -;  
DR HSSP; P42771; 1BI7.  
DR PFAM; PF00023; ank; 3.  
KW Kinase; Cyclin.  
SQ SEQUENCE 168 AA; 17915 MW; F0087F4C CRC32;  
  
Query Match 99.8%; Score 890; DB 11; Length 168;  
Best Local Similarity 99.2%; Pred. No. 5.44e-185;  
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Db 44 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAG 103  
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAG 60  
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Db 104 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 163  
QY 61 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120  
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Db 164 SQEQS 168  
QY 121 SQEQS 125  
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RESULT 3 PRELIMINARY; PRT; 113 AA.  
ID Q921C2  
AC Q921C2;  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
GN P16.  
OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRET/EI;  
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,  
RA PELLICER A., FERNANDEZ-PIQUERAS J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U79634; AAD00236.1; -;  
DR HSSP; P42771; 1BI7.  
DR NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 113 AA; 12073 MW; 1D82E6DF CRC32;  
  
Query Match 90.4%; Score 806; DB 11; Length 113;  
Best Local Similarity 100.0%; Pred. No. 3.20e-164;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60  
Db 62 RLPDLDAERGHQDIVYRLSAGCSAGWSLCTAGNVAQTDGHSFSSSTP 113  
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QY 61 RLPDLDAERGHQDIVYRLSAGCSAGWSLCTAGNVAQTDGHSFSSSTP 112

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AC Q9XS51;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE P16/CDKN2A/MTS1 (FRAGMENT).  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=PBMC;  
RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,  
RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;  
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)  
RT and p15(MTS2/CDKN2B).";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB010807; BAA33540.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 102 AA; 10824 MW; 8C3094E9 CRC32;

Query Match 55.2%; Score 492; DB 6; Length 102;  
Best Local Similarity 79.0%; Pred. No. 7.62e-88;  
Matches 64; Conservative 11; Mismatches 6; Indels 0; Gaps 0;  
Db 2 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 61  
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QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60  
Db 62 RLPDLDAERGHQDIVYRLSAG 82  
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QY 61 RLPDLDAERGHQDIVYRLSAG 81

RESULT 5  
ID Q9XS52 PRELIMINARY; PRT; 86 AA.  
AC Q9XS52;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE P15/MTS2/CDKN2B (FRAGMENT).  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=PBMC;  
RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,  
RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;  
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)  
RT and p15(MTS2/CDKN2B).";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB010808; BAA33541.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 86 AA; 9340 MW; 8C5D01A0 CRC32;

Query Match 54.7%; Score 488; DB 6; Length 86;  
Best Local Similarity 75.9%; Pred. No. 6.86e-87;  
Matches 63; Conservative 13; Mismatches 7; Indels 0; Gaps 0;  
Db 2 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 61  
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QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60

Db 62 RLPVDLAERGHQDIVYRLRAAA 84  
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QY 61 RLPDLDAERGHQDIVYRLSAG 83  
RESULT 6  
ID Q16361 PRELIMINARY; PRT; 115 AA.  
AC Q16361;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE CELL CYCLE NEGATIVE REGULATOR BETA FORM (FRAGMENT).  
GN P16/MTS1/CDKN2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 9530726.  
RA STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,  
RA PARRY D., PETERS G., KAMB A.;  
RT "Complex structure and regulation of the p16 (MTS1) locus.";  
RL Cancer Res 55:2988-2994(1995).  
DR EMBL; S78535; AAC60650.1; -.  
DR HSP; P42771; IBI7.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 115 AA; 12334 MW; F5BEF54B CRC32;

Query Match 53.0%; Score 473; DB 4; Length 115;  
Best Local Similarity 73.5%; Pred. No. 2.55e-83;  
Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
Db 11 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 70  
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QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60  
Db 71 RLPVDLAERGHQDIVYRLRAAA 93  
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QY 61 RLPDLDAERGHQDIVYRLSAG 83

RESULT 7  
ID Q921C1 PRELIMINARY; PRT; 86 AA.  
AC Q921C1;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
GN P15.  
OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=SPRET/EI;  
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,  
RA PELLICER A., FERNANDEZ-PIQUERAS J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
RT in mouse inbred strains.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U79637; AAD00237.1; -.  
DR HSP; P42771; IBI7.  
KW Kinase; Cyclin.  
FT NON\_TER 1  
FT NON\_TER 86  
SQ SEQUENCE 86 AA; 9269 MW; D5811BE2 CRC32;

Query Match 51.7%; Score 461; DB 11; Length 86;  
Best Local Similarity 73.2%; Pred. No. 1.80e-80;  
Matches 60; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
Db 2 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 61

KW	kinase; Cyclin.	1	
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FT	NON_TER	58	
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Query Match			24.0%; Score 214; DB 6; Length 58;



Best Local Similarity 75.08; Pred. No. 2.98e-24; Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 19 MMGSVHVAELLHLLGADPNRDPDTLRPVHDAAREGFL 58  
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFL 40

RESULT 12  
 ID Q9Y2V6 PRELIMINARY; PRT; 835 AA.  
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 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)  
 DE HYPOTHETICAL 92.9 KD PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART;  
 RA WEI Y.J., DING J.F., XIONG H., ZHOU Y., HUI R.T., LIEW C.C.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF116826; AAD29632.1; -.  
 KW Hypothetical protein  
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 Matches 30; Conservative 19; Mismatches 26; Indels 3; Gaps 3;

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 QY 4 GNHVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLD-T-LVYLHSGARLDVYDWA 61

Db 237 VPLHFCRSRFGHHDIVYL 254  
 QY 62 LPDLAQERGHQDIVRYL 79

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 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)  
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 GN NOTCH1 OR MT14.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MESSERLE M., FOLIO M., NEHLS M., EGGERT H., BOEHM T.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X82562; CAA57909.1; -.  
 DR HSSP: Q00421; IAWC.  
 DR MGD: MGI:97363; Notch1.  
 DR PFAM: PF00023; ank; 4.  
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Db 136 LPDLAQERGHQDIVRYL 153  
 QY 62 LPDLAQERGHQDIVRYL 79

Best Local Similarity 75.08; Pred. No. 2.98e-24; Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFL 40

RESULT 12  
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 AC Q9Y2V6;  
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART;  
 RA WEI Y.J., DING J.F., XIONG H., ZHOU Y., HUI R.T., LIEW C.C.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF116826; AAD29632.1; -.  
 KW Hypothetical protein  
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Query Match 18.38; Score 163; DB 4; Length 835;  
 Best Local Similarity 38.58; Pred. No. 8.57e-14;  
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Db 178 GHQVTRLLKFGADVNVSGEVG-DRLPLHLSAKGFLNIAKLLMEESKADVNAQDNEDH 236  
 QY 4 GNHVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLD-T-LVYLHSGARLDVYDWA 61

Db 237 VPLHFCRSRFGHHDIVYL 254  
 QY 62 LPDLAQERGHQDIVRYL 79

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 ID Q61905 PRELIMINARY; PRT; 251 AA.  
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 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)  
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 GN NOTCH1 OR MT14.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
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 RA MESSERLE M., FOLIO M., NEHLS M., EGGERT H., BOEHM T.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X82562; CAA57909.1; -.  
 DR HSSP: Q00421; IAWC.  
 DR MGD: MGI:97363; Notch1.  
 DR PFAM: PF00023; ank; 4.  
 FT NON\_TER 1 1  
 FT NON\_TER 251 251  
 SQ SEQUENCE 251 AA; 27087 MW; D5FBAB3C CRC32;

Query Match 17.98; Score 160; DB 11; Length 251;  
 Best Local Similarity 43.68; Pred. No. 3.33e-13;  
 Matches 34; Conservative 13; Mismatches 28; Indels 3; Gaps 3;

Db 78 VNNVDAAVLLKNGAKDMONKE-ETPLFLAAREGSYETAKVLLDHFGR-DITDHMR 135  
 QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLD-T-LVYLHSGARLDVYDWA 61

Db 136 LPDLAQERGHQDIVRYL 153  
 QY 62 LPDLAQERGHQDIVRYL 79

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VERSION 189920.1 GI:3409860
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 713)
  Sherr,C.J. and Quelle,D.E.
  ARF-p19, a novel regulator of the mammalian cell cycle
  JOURNAL Patent: US 5723313-A 1 03-MAR-1998;
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    1 (bases 1 to 713)
    Quelle,D.E., Zindy,F., Ashmun,R.A. and Sherr,C.J.
    Alternative reading frames of the INK4a tumor suppressor gene
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LOCUS S80650 713 bp mRNA ROD 02-APR-1996  
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 erythroleukemia cells, mRNA Partial, 713 nt].  
 S80650  
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 VERSION Cell 83 (6), 993-1000 (1995)  
 KEYWORDS S80650.1 GI:1245977  
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 ORGANISM Mus sp.  
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 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 713)  
 AUTHORS Queller, D.E., Zindy, F., Ashmun, R.A. and Sherr, C.J.  
 TITLE Alternative reading frames of the INK4a tumor suppressor gene  
 encode two unrelated proteins capable of inducing cell cycle arrest  
 Cell 83 (6), 993-1000 (1995)  
 JOURNAL 9610737  
 MEDLINE  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 174807] from the original journal article.  
 This sequence comes from Fig. 2.  
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 seq\_documentation\_block:  
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 DEFINITION Mus musculus CDK4 and CDK6 inhibitor protein (p16INK4a) mRNA,  
 complete cds.  
 ACCESSION L76150  
 VERSION L76150.1 GI:1162948  
 KEYWORDS CDK4 inhibitor; CDK6 inhibitor.  
 SOURCE Mus musculus cDNA to mRNA.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 846)  
 AUTHORS Queller, D.E., Ashmun, R.A., Hannon, G.J., Rehberger, P.A., Trono, D.,  
 Richter, K.H., Walker, C., Beach, D., Sherr, C.J. and Serrano, M.  
 TITLE Cloning and characterization of murine p16INK4a and p15INK4b genes  
 JOURNAL Oncogene 11 (4), 635-645 (1995)  
 MEDLINE 95380169  
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seq\_documentation\_block:  
 LOCUS AF044336 849 bp mRNA ROD 01-APR-1998  
 DEFINITION Mus musculus strain DBA/2N cyclin dependent kinase inhibitor  
 p16INK4a (Cdkn2a) mRNA, complete cds.  
 ACCESSION AF044336  
 VERSION AF044336.1 GI:3002948  
 KEYWORDS house mouse.  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS Zhang, S., Ramsay, E.S. and Mock, B.A.  
 TITLE Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a)  
 and p19(ARF), is a candidate for the plasmacytoma susceptibility  
 locus, pctl1  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)  
 MEDLINE 98151529  
 REFERENCE 2 (bases 1 to 849)  
 AUTHORS Zhang, S., Ramsay, E.S. and Mock, B.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JAN-1998) NCI/IG, NIH, 37 Convent Dr., Bethesda, MD  
 20892, USA

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BASE COUNT  
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 p16INK4a (Cdkn2a) mRNA, complete cds.  
 ACCESSION AF044336  
 VERSION AF044335.1 GI:3002946  
 KEYWORDS house mouse.  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS Zhang, S., Ramsay, E.S. and Mock, B.A.  
 TITLE Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a)  
 and p19(ARF), is a candidate for the plasmacytoma susceptibility  
 locus, pctl1  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)  
 MEDLINE 98151529  
 REFERENCE 2 (bases 1 to 849)  
 AUTHORS Zhang, S., Ramsay, E.S. and Mock, B.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JAN-1998) NCI/IG, NIH, 37 Convent Dr., Bethesda, MD  
 20892, USA  
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561 TCGGGGCCAATCCCAAGACGACAGC 585

seq_name: gb_ro:MMINK4A02
seq documentation_block:
LOCUS MMINK4A02 482 bp DNA ROD 02-JAN-1997
DEFINITION Mus musculus cyclin-dependent kinase inhibitor (p16INK4a) gene,
exon 2 and partial cds.
ACCESSION U66087
VERSION U66087.1 GI:1762922
KEYWORDS
SEGMENT 2 of 2
SOURCE house mouse.

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 482)
AUTHORS Malumbres,M., Perez de Castro,I., Santos,J., Melendez,B.,
Manques,R., Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE Inactivation of the cyclin-dependent kinase inhibitor p16INK4a by
deletion and de novo methylation with independence of p16INK4a
alterations in murine primary T-cell lymphomas
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 482)
AUTHORS Malumbres,M. and Pellicer,A.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1996) Pathology (MSB 594), New York University
Medical Center, 550 First Avenue, New York, NY 10016, USA
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67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100

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204 CCACAGCGGGGACATCAACACATCGTCCGATATTGCGTCCGCTGGGT 253

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seq\_documentation\_block: 339 bp DNA ROD 05-JAN-1999

LOCUS MSU79634 Mus spretus cyclin-dependent kinase inhibitor protein (p16(INK4a))

DEFINITION gene, exon 2 and partial cds.

ACCESSION U79634

VERSION U79634.1 GI:4098165

KEYWORDS western wild mouse.

SOURCE Mus spretus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 339)

AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,

Serrano, M., Pellicer, A., and Fernandez-Piqueras, J.

TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

JOURNAL in mouse inbred strains

REFERENCE 2 (bases 1 to 339)

AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,

Serrano, M., Pellicer, A., and Fernandez-Piqueras, J.

TITLE Direct Submission

JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,

Cantoblanco, Madrid, Madrid 28049, Spain

FEATURES Location/Qualifiers

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seq\_documentation\_block: 339 bp DNA ROD 05-JAN-1999

LOCUS MMU79633 Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))

DEFINITION gene, exon 2 and partial cds.

ACCESSION U79633

VERSION U79633.1 GI:4098153

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 339)

AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,

Serrano, M., Pellicer, A., and Fernandez-Piqueras, J.

TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

JOURNAL in mouse inbred strains

REFERENCE 2 (bases 1 to 339)

AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,

Serrano, M., Pellicer, A., and Fernandez-Piqueras, J.

TITLE Direct Submission

JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,

Cantoblanco, Madrid, Madrid 28049, Spain

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US-09-016-869a-6 x MSU79634

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1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17

4 ATGATGATGGGCAACGCTTTCACATAGCAGCTCTCTGCTCAACTACGGTGC 53

17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34

|||||  
54 AGATTTCGAACTCGGAGGCCACCTACCTTCTCCCGCGCGGTGCACGACG 103









84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValala 100  
 380 GCTCTTTGTTCCGCTGGTGGTCTTTGTGTACCGCTGGGAACGTCGCC 429  
 101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117  
 430 CAGACCGAGCGGCATAGCTTCAGTCAAGCACGCCGAGGCGCTGGAAC 479  
 117 uArgGlyGlnSerGlnGluGlnSer 125  
 480 TCGCGGCCAATCCAGACGACGAGC 504

seq\_name: N\_Geneseq\_36:T62485

seq\_documentation\_block:

ID T62485 standard; CDNA; 713 BP.  
 AC T62485;  
 DT 16-AUG-1997 (first entry)  
 DE Murine ARF-p19 CDNA.  
 KW ARF-p19; alternative reading frame; cell cycle; cancer; diagnosis;  
 KW gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6;  
 KW inhibitor; ss.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT cds 43..552  
 FT /\*tag= a  
 FT /product= ARF-p19  
 FT cds 236..613  
 FT /\*tag= b  
 FT /product= INK4a-p16 C-terminal fragment  
 FT exon 1..232  
 FT /\*tag= c  
 FT /note= "Exon 1-beta"  
 FT exon 233..702  
 FT /\*tag= d  
 FT /note= "Exon 2"  
 FT primer\_bind complement(56..75)  
 FT /\*tag= e  
 FT /note= "5' primer for RT-PCR"  
 FT primer\_bind 602..624  
 FT /\*tag= f  
 FT /note= "3' primer for RT-PCR"  
 WO9712060-A1.

PN 03-APR-1997.  
 PD 25-SEP-1996; U15312.  
 PF 27-SEP-1995; US-534975.  
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
 PI Quelle DE, Sherr CJ;  
 DR WPI; 97-212919/19.  
 DR P-PSDB; W16321-22.  
 PT Nucleic acid encoding ARF-p19 which induces cell cycle arrest when  
 PT overexpressed - used for diagnosis and treatment of cancer, and for  
 PT drug screening  
 PS Claim 2; Fig 1; 49pp; English.  
 CC A murine CDNA molecule (T62485) homologous to human INK4A beta  
 CC transcripts (see also T62486) was isolated from a mouse  
 CC erythroleukaemia cell DNA library. Sequences of exon 1-beta are  
 CC spliced to exon 2 to create an open reading frame that encodes a  
 CC novel protein, ARF-p19 (W16321), which induces cell cycle arrest  
 CC when overexpressed. Unrelated sequences from exon 1-alpha (not  
 CC shown) are spliced to the same exon 2 acceptor site to open another  
 CC reading frame that encodes INK4a-p16 (C-terminal fragment given in  
 CC W16322), an inhibitor of the cyclin D-dependent kinases CDK4 and  
 CC CDK6. Economical reutilisation of protein coding sequences in this  
 CC manner is without precedent in mammalian genomes and the unitary  
 CC inheritance of INK4a-p16 and ARF-p19 may reflect a dual requirement  
 CC for both proteins in cell cycle control. ARF-p19 nucleic acids can  
 CC be used as probes or primers, or in gene therapy protocols to  
 CC induce cell arrest in eukaryotes or (antisense) to inhibit ARF-p19  
 CC activity, and to create transgenic animals useful as models for  
 CC cancer. Human ARF-p19 CDNA (T62486) has also been isolated.  
 CC Sequence 713 BP; 133 A; 195 C; 223 G; 162 T;

alignment\_scores:  
 Quality: 658.00 Length: 125  
 Ratio: 5.264 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-016-869A-6 x T62485 ..  
 Align seg 1/1 to: T62485 from: 1 to: 713  
 1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17  
 236 ATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGCTGC 285  
 17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34  
 286 AGATTTCGAATCGGAGGACCCCACTACCTTCTCCCGCCGGTGCACGACG 335  
 34 laaAaargGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50  
 336 CAGCGCGGGAAGGCTTCCTGGACACGCTGGTGGTGTGCACGGGTGAGGG 385  
 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67  
 386 GCTCGGCTGGATGTGGCGGATGCTGGGGTGGCTGCGCTCGCTGACTTGC 435  
 67 aGlnGluAtrgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84  
 436 CCAGAGCGGGGACATCAAGACATCGTGGCATATTTGCGTTCCGCTGGGT 485  
 84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValala 100  
 486 GCCTTTGTGTTCCGCTGGTGGTGGTCTTTGTGTACCGCTGGGACGTCGCC 535  
 101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117  
 536 CAGACCGAGCGGCATAGCTTCAGTCAAGCACGCCGAGGCGCTGGAAC 585  
 117 uArgGlyGlnSerGlnGluGlnSer 125  
 586 TCGCGGCCAATCCAGACGACGAGC 610  
 seq\_name: N\_Geneseq\_36:T02965

seq\_documentation\_block:

ID T02965 standard; CDNA; 853 BP.  
 AC T02965;  
 DT 01-MAR-1996 (first entry)  
 DE Cell-cycle regulatory protein p13.5 CDNA.  
 KW Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;  
 KW CCR; gene therapy; transgenic animal; cancer; cell proliferation;  
 KW ss; ds.  
 OS Mus sp.  
 FH Key Location/Qualifiers  
 FT cds 213..590  
 FT /\*tag= a  
 PN WO9528483-A1.  
 PD 26-OCT-1995.  
 PF 14-APR-1995; U04536.  
 PR 14-APR-1994; US-227371.  
 PR 25-MAY-1994; US-248812.  
 PR 14-SEP-1994; US-306511.  
 PR 29-NOV-1994; US-346147.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PI Beach DH, Demetrick DU, Hannon GJ, Serrano M;  
 DR WPI; 95-373798/48.  
 DR P-PSDB; R85120.  
 PT New cell cycle regulating proteins bind to cyclin dependent kinase -  
 PT and related nucleic acids, antibodies etc., used in diagnosis and  
 PT therapy of abnormal cell proliferation, degeneration etc.  
 PT Example 4; Page 80; 109pp; English.

CC cDNA (T02965) coding for the mouse cell-cycle regulatory (CCR)  
 CC protein p13.5 (R85120) was isolated from an embryonal stem cell  
 CC The isolated cDNA based on human CCR p16 cDNA (T02962).  
 CC library using a probe based on human CCR p16 cDNA (T02962).  
 CC The isolated cDNA can be used to detect mutations in CCR  
 CC genes that lead to cell proliferation; to breed transgenic  
 CC animals to study cellular disorders involving CCR allele  
 CC mutation/misexpression; and to correct CCR-deficient cells  
 CC (gene therapy).  
 SQ Sequence 853 BP: 192 A: 207 C: 274 G: 180 T:

alignment\_scores:  
 Quality: 558.00 Length: 125  
 Ratio: 5.264 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-016-869A-6 x T02965

Align seg 1/1 to: T02965 from: 1 to: 853

```

1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
|||||
213 ATGATGATGGCAACGTTACGTAGCAGCTTCTGCTCAACTACGGTGC 262

17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
263 AGATTCAACTGCGAGGACCCACTACTCTTCCCGCCGGTGCACGACG 312

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
313 CAGCGCGGGAAGGCTTCTCGACACGCTGGTGTGCTGCACGGGTACGGG 362

51 AlaArgLeuAspValArgAspAlaTirPlyArgLeuProLeuAspLeuAl 67
|||||
363 GCTCGGCTGGATGTCGCGATGCTCGGGGTGCGCTCGCGCTGACATTGGC 412

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
413 CCAAGAGCGGGGACATCAAGACATCGTGCATATTTGCGTTCCGCTGGGT 462

84 ySerLeuCySerAlaGlyTirPserLeuCyThrAlaGlyAsnValAla 100
|||||
463 GCTCTTTGTGTTCGCTGGGTGGTGTGTGTGTACCGCTGGGAACGTCGCC 512

101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
|||||
513 CAGACCCAGCGGCATAGCTTCAGCTCAAGCAGCCAGGGGCCCTGGAACT 562

117 uArgGlyGlnSerGlnGlnSer 125
|||||
563 TCGCGGCAATCCCAAGACGACAGC 587

```

seq\_name: N\_Geneseq\_36.V11259

seq\_documentation\_block:

ID V11259 standard; cDNA; 395 BP.  
 AC V11259;  
 DT 15-JUL-1998 (first entry)  
 DE Mouse p16 cDNA fragment.  
 KW MTS1; MTS2; MTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;  
 KW germ-line mutation; familial melanoma locus; MLM; predisposition; ds.  
 OS Mus sp.  
 PN US5739027-A.  
 PD 14-APR-1998.  
 PF 07-JUN-1995; 487033.  
 PR 07-JUN-1995; US-487033.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.  
 PI Kamb A;  
 DR WPI; 98-250421/22.  
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are  
 PT useful for the diagnosis of cancers related to MTS1E1-beta  
 PT mutation(s) and their treatment  
 PS Disclosure; Figure 14; 72pp; English.  
 CC This is a mouse p16 cDNA sequence used in the characterisation of the  
 CC human multiple tumour suppression proteins, MTS1, MTS2 and MTS1E1-beta.  
 CC The MTS gene locus is also referred to as the familial melanoma (MLM)  
 CC gene locus, located on human chromosome 9p21. Germ line mutations in  
 CC MTS genes can be used in the diagnosis of predisposition to cancers.  
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,  
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,  
 CC ovary, uterus, testis, kidney, stomach and rectum.  
 SQ Sequence 395 BP: 73 A: 109 C: 128 G: 85 T:

alignment\_scores:

Quality: 445.00 Length: 85  
 Ratio: 5.235 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.824

alignment\_block:

US-09-016-869A-6 x V11259

Align seg 1/1 to: V11259 from: 1 to: 395

```

1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
|||||
140 ATGATGATGGCAACGTTACGTAGCAGCTTCTGCTCAACTACGGTGC 189

17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
190 AGATTCAACTGCGAGGACCCACTACTCTTCCCGCCGGTGCACGACG 239

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
240 CAGCGCGGGAAGGCTTCTCGACACGCTGGTGTGCTGCACGGGTACGGG 289

51 AlaArgLeuAspValArgAspAlaTirPlyArgLeuProLeuAspLeuAl 67
|||||
290 GCTCGGCTGGATGTCGCGATGCTCGGGGTGCGCTCCCGCTCGACTCGC 339

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
340 CCAAGAGCGGGGACATCAAGACATCGTGCATATTTGCGTTCCGCTGGGT 389

84 ySer 85
|||||
390 GCTCT 394

```

seq\_name: N\_Geneseq\_36.V53840

seq\_documentation\_block:

ID V53840 standard; DNA; 395 BP.  
 AC V53840;  
 DT 04-DEC-1998 (first entry)  
 DE Nucleotide sequence of nucleic acid 6.  
 KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;  
 KW somatic mutation; gene therapy; ds.  
 OS Homo sapiens.  
 PN US5801236-A.  
 PD 01-SEP-1998.  
 PF 07-JUN-1995; 480810.  
 PR 07-JUN-1995; US-480810.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215086.  
 PR 18-MAR-1994; US-215087.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PR 17-MAR-1995; WO-U03316.  
 PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;  
DR WPI; 98-494842/42.  
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
PS Disclosure; Column 83-84; 73pp; English.  
CC This is the nucleotide sequence of a nucleic acid used in the  
CC method of the invention involving the use of the multiple tumour  
CC suppressor (MTS) gene to diagnose and treat human cancers. The MTS  
CC gene is useful in the diagnosis and prognosis of human cancer, e.g.  
CC by standard nucleic hybridisation techniques, of patient samples.  
CC The mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.  
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

alignment\_scores:  
Quality: 445.00 Length: 85  
Ratio: 5.235 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.824

alignment\_block:  
US-09-016-869A-6 x V53840 ..

Align seg 1/1 to: V53840 from: 1 to: 395

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1 MetMetMetClyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
|||||
140 ATGATGATGGGCAAGCTTCACGTACGACTCTTCGTCACTACGAGTGC 189

17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
190 AGATTGCAACTCGAGGACCCCACTACCTTCTCCCGCCGGTGCAGGAC 239

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
240 CAGCGCGGCAAGGCTTCTCTGGACACGCTGGTGTCTGCACGGGTACGG 289

51 AlaArgLeuAspValArgAspAlaTyrGlyArgLeuProLeuAspLeuAl 67
|||||
290 GCTCGCTGGATGTCGCGATGCTCGGGTGGCTCCCTCCGCTCGACTTCGC 339

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
340 CCAAGAGCGGGGACATCAAGACATCGTCGATATTGCGTTCCGCTGGGT 389

84 ySser 85
|||||
390 GCTCT 394
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seq\_name: N\_Geneseq\_36:V70604

seq\_documentation\_block:  
ID V70604; standard; cDNA; 395 BP.  
AC V70604;  
DT 03-FEB-1999 (first entry)  
DE cDNA encoding a murine multiple tumour suppressor 1 gene; MTS1; cancer; ds.  
KW Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ds.  
OS Mus SP.  
PN US5843756-A.  
PD 01-DEC-1998.  
PF 28-JUL-1995; 058735.  
PR 28-JUL-1995; US-508735.  
PR 07-JUN-1995; US-487033.  
PA (MYRI-) MYRIAD GENETICS INC.  
PI Jiang P, Kamb A, Stone S;

DR WPI; 99-044585/04.  
PT Mouse multiple tumour suppressor gene segment - useful for primer  
PT design  
PS Example 8; Fig 14; 80pp; English.  
CC The present sequence encodes murine multiple tumour suppressor 1E1-beta  
CC (Mts1E1-beta) protein. Primers designed from the gene can be used to  
CC design primers to detect abnormalities i.e. polymorphisms which may  
CC predispose towards malignancies such as melanoma, leukaemia,  
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,  
CC thyroid, pancreas, uterus and kidneys.  
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

alignment\_scores:  
Quality: 445.00 Length: 85  
Ratio: 5.235 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.824

alignment\_block:  
US-09-016-869A-6 x V70604 ..

Align seg 1/1 to: V70604 from: 1 to: 395

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1 MetMetMetClyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
|||||
140 ATGATGATGGGCAAGCTTCACGTAGCAGCTTCTGCTCACTACGAGTGC 189

17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
190 AGATTGCAACTCGAGGACCCCACTACCTTCTCCCGCCGGTGCAGGAC 239

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
240 CAGCGCGGCAAGGCTTCTCTGGACACGCTGGTGTCTGCACGGGTACGG 289

51 AlaArgLeuAspValArgAspAlaTyrGlyArgLeuProLeuAspLeuAl 67
|||||
290 GCTCGCTGGATGTCGCGATGCTCGGGTGGCTCCCTCCGCTCGACTTCGC 339

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
340 CCAAGAGCGGGGACATCAAGACATCGTCGATATTGCGTTCCGCTGGGT 389

84 ySser 85
|||||
390 GCTCT 394
```

seq\_name: N\_Geneseq\_36:T00739

seq\_documentation\_block:  
ID T00739 standard; DNA; 1187 BP.  
AC T00739;  
DT 08-MAY-1996 (first entry)  
DE Multiple tumour suppressor 1 (MTS1) gene exon 2 contg. fragment.  
KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;  
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;  
KW pancreas; breast; thyroid; exon 2; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT intron 1..191  
FT /tag= a  
FT /label= intron 2  
FT exon 192..498  
FT /tag= b  
FT /label= exon 2  
FT intron 499..1187  
FT /tag= c  
FT /label= intron 3  
PN WO9525813-A1.  
PD 28-SEP-1995.  
PF 17-MAR-1995; U03537.  
PR 18-MAR-1994; US-214582.  
PR 18-MAR-1994; US-215087.

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PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 95-344626/44.
PT Detecting polymorphism associated with cancer pre-disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Claim 13; Pages 94-95; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to exon 1
CC (T00737) or exon 2 (T00739) of the MTS1 gene. The above assay can
CC also be used in the diagnosis and prognosis of melanoma, lymphoma,
CC leukaemia and pancreas, breast and thyroid cancers, etc.
SQ Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

alignment_scores:
  Quality: 338.50      Length: 139
  Ratio: 3.319        Gaps: 2
  Percent Similarity: 73.381 Percent Identity: 52.518

alignment_block:
  US-09-016-869A-6 x T00739 ..
  Align seg 1/1 to: T00739 from: 1 to: 1187

1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
195 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGGCGC 244

17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
245 GGACCCCACTGCGCCAGCCCGCCATCTCACCCGACCGCTGGACGACG 294

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
295 CTGCGCGGAGGGCTTCTCTGACACGCTGCTGCTGCTGACCGCGCGG 344

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
345 GCGCGGCTGGACGCGCGATGCTGCGGCGCTGCTGCGGCGGACCTGGC 394

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
395 TGAGGAGCTGGGCCATCGCGATGTCGACGCTACCTGCGCGCGCTGGC 444

84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly..... 97
445 GGGCACCAGAGCGAGTAACCATGCCGCTAGATGCCGCGAAGGTCCC 494

98 .....AsnValAlaGlnTh 102
495 TCAGGTGAGGACTGATGATCTGAGAAATTGTGACCTGAGACTTCCAAAG 544

102 rAspGlyHisSerPheSerSer.....SerThrProArgAlaLeuGluL 117
545 CTCAGAGCATTCATTTCCACAGCAGAAAGTTCAGCCCGGAGACCACTC 594

117 euArgGlyGlnSerGln 122
595 TCCGGTCTTGGCTCAG 611

seq_name: N_Genseq_36.V11240

seq_documentation_block:
ID V11240 standard; DNA; 1187 BP.
AC V11240;
DT 15-JUL-1998 (first entry)
DE Human MTS1 genomic DNA including exon 2.
```

```
KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition; ds.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..1187
FT /tag= a
FT /product= MTS1
FT /note= "partial coding region of multiple tumour
FT suppressor protein which is interrupted by
FT introns 1 and 2"
FT intron 1..191
FT /tag= b
FT /number= 1
FT exon 192..498
FT /tag= c
FT /number= 2
FT intron 499..1187
FT /tag= d
FT /number= 2
FT
PN US739027-A.
PD 14-APR-1998.
PE 07-JUN-1995; 487033.
PR 07-JUN-1995; US-487033.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 98-250421/22.
DR P-PSDB; W40524.
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PT Disclosure; Fig 6; 72pp; English.
PS This sequence encodes the human multiple tumour suppression protein,
CC MTS1, exon 2. The MTS gene locus is also referred to as the familial
CC melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line
CC mutations in MTS genes can be used in the diagnosis of predisposition to
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, kidney, stomach and rectum.
SQ Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

alignment_scores:
  Quality: 338.50      Length: 139
  Ratio: 3.319        Gaps: 2
  Percent Similarity: 73.381 Percent Identity: 52.518

alignment_block:
  US-09-016-869A-6 x V11240 ..
  Align seg 1/1 to: V11240 from: 1 to: 1187

1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
195 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGGCGC 244

17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
245 GGACCCCACTGCGCCAGCCCGCCATCTCACCCGACCGCTGGACGACG 294

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
295 CTGCGCGGAGGGCTTCTCTGACACGCTGCTGCTGCTGACCGCGCGG 344

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
345 GCGCGGCTGGACGCGCGATGCTGCGGCGCTGCTGCGGCGGACCTGGC 394
```

```

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
139 TGGAGGAGCTGGGCGGATGCGGATGCGACGGTACCTGCGCGCGGTGGG 444
84 ysSerLeuCysSerAlaGlyTyrPheLeuArgTyrLeuArgSerAlaGlyC 97
445 GGGGACACAGAGCAGTACCATGCCCGCATAGATGCCGCGGAAGTCCC 494
98 .....
495 TCAGGTGAGGACTGATGATCTGAGAAATTTGTACTCTGAGAGCTTCCAAAG 544
102 rAspGlyHisSerPheSer.....SerThrProArgAlaLeuGluL 117
545 CTCAGAGCATTCATTTTCAGCAGACAGAAAGTTTCAGCCCGGAGACCATGTC 594
117 euArgGlyGlnSerGln 122
595 TCCGGTCTTCGCTCAG 611

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seq\_name: N\_Geneseq\_36:V53821

seq\_documentation\_block:

ID V53821 standard; cDNA; 1187 BP.

AC V53821:

DT 04-DEC-1998 (first entry)

DE Coding sequence 2 of the multiple tumour suppressor 1.

KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;

KW somatic mutation; gene therapy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT intron

FT 1..191

FT /\*tag= a

FT /note= "intron 1"

FT exon

FT 192..498

FT /\*tag= b

FT /note= "exon 1"

FT intron

FT 499..1187

FT /\*tag= c

FT /note= "intron 2"

FT US5801236-A.

PD 01-SEP-1998.

PF 07-JUN-1995; 480810.

PR 07-JUN-1995; US-480810.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-494842/42.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -

PT useful as hybridisation probes, primers and recombinant production

PT of MTS in the diagnosis and treatment of cancers related to MTS

PT mutation(s)

PS Claim 1; Fig 6A-6B; 73pp; English.

CC This is the nucleotide sequence of the multiple tumour suppressor 1

CC (MTS-1) gene, used in the method of the invention. The MTS gene

CC is useful in the diagnosis and prognosis of human cancer, e.g. by

CC standard nucleic hybridisation techniques, of patient samples. The

CC mutated sequences are those that are present in somatic mutations

CC of the gene in cancers. The vectors can be used for gene therapy

CC strategies to replace function of mutated protein in patients. These

CC can also be used to construct protein mimetics, also for therapeutic

CC strategies. In addition the expression constructs can also be used

CC for recombinant production of MTS. Recombinant MTS can be used to

CC screen for drugs to be used for cancer therapy, and the protein

CC itself may also be used to restore MTS function in a cell.

CC Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

SO

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  Ratio: 3.319        Gaps: 2
  Percent Similarity: 73.381  Percent Identity: 52.518

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295 CTGCGCGGAGGCTTCTCTGGACACGCTGGTGTGTGCACCGGCGCGG 344
51 AlaArgLeuAspValArgAspAlaTyrGlyArgLeuProLeuAspLeuAl 67
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67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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445 GGGGACACAGAGCAGTACCATGCCCGCATAGATGCCGCGGAAGTCCC 494
98 .....
495 TCAGGTGAGGACTGATGATCTGAGAAATTTGTACTCTGAGAGCTTCCAAAG 544
102 rAspGlyHisSerPheSer.....SerThrProArgAlaLeuGluL 117
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117 euArgGlyGlnSerGln 122
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seq\_name: N\_Geneseq\_36:V70585

seq\_documentation\_block:

ID V70585 standard; DNA; 1187 BP.

AC V70585;

DT 03-FEB-1999 (first entry)

DE Human multiple tumour suppressor 1 (MTS1) DNA fragment.

KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT intron

FT 1..191

FT /\*tag= a

FT exon

FT 192..498

FT /\*tag= b

FT intron

FT 499..1187

FT /\*tag= c

PN US5843756-A.

PD 01-DEC-1998.

PF 28-JUL-1995; 058735.

PR 28-JUL-1995; US-508735.

PR 07-JUN-1995; US-487033.

PA (MYRI-) MYRIAD GENETICS INC.

PI Jiang P, Kamb A, Stone S;

DR WPI; 99-044585/04.

PT Mouse multiple tumour suppressor gene segment - useful for primer

PT design

PS Example 6; Fig 6A-B; 80pp; English.



CC The present sequence represents part of intron 1, exon 2 and part  
 CC of intron 2 for a human multiple tumour suppressor 1 (MTS1) gene. The  
 CC MTS1 sequence is homologous to the corresponding murine gene.  
 CC Primers designed from the gene can be used to design primers to  
 CC detect abnormalities i.e. polymorphisms which may predispose towards  
 CC malignancies such as melanoma, leukaemia, astrocytoma, lymphoma,  
 CC glioma, as well as tumours of e.g. the breast, thyroid, pancreas,  
 CC uterus and kidneys.  
 SQ Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

alignment\_scores:  
 Quality: 338.50 Length: 139  
 Ratio: 3.319 Gaps: 2  
 Percent Similarity: 73.381 Percent Identity: 52.518

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Align seg 1/1 to: V70585 from: 1 to: 1187

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34 laAlaArgGluGlyPheLeuAspThrLeuValLeuHisGlySerGly 50
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395 TGAGGAGCTGGCGCATCGCATGTCGACGCTACCTGCGCGCGCTGGG 444

84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly..... 97
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595 TCCGGTCTTGGCGTCAG 611

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seq\_name: N\_Geneseq\_36:T00747

seq\_documentation\_block:

ID T00747 standard; cDNA; 947 BP.

AC T00747;  
 DT 08-MAY-1996 (first entry)  
 DE Multiple tumour suppressor 1 (MTS1) cDNA.  
 KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;  
 KW predisposition; melanoma; leukaemia; lymphoma; prognosis;  
 KW pancreas; breast; thyroid; ds.  
 OS Homo sapiens.

FH key Location/Qualifiers

FT misc\_feature 151

FT /\*tag= a

FT /note= "splice site acceptor"

FT misc\_feature 458

FT /\*tag= b

FT /note= "splice site acceptor"

PN WO9525813-Al.  
 PD 28-SEP-1995.  
 PF 17-MAR-1995; U03537.  
 PR 18-MAR-1994; US-214582.  
 PR 18-MAR-1994; US-215087.  
 PR 18-MAR-1994; US-215086.  
 PR 14-APR-1994; US-227369.  
 PR 01-JUN-1994; US-251938.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 PI Cannon-Albright LA, kamb A, Skolnick MH;  
 DR WPI; 95-344626/44.  
 PT Detecting polymorphism associated with cancer pre-disposition - also  
 PT DNA, vectors and host cells e.g. for gene or protein replacement  
 PT therapy and drug screening  
 PS Disclosure: Pages 111-112; 148pp; English.  
 CC An individual can be diagnosed as having a predisposition to cancer  
 CC by detecting an alteration in the wild type multiple tumour  
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1  
 CC cDNA T00747. The above assay can also be used in the diagnosis and  
 CC prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and  
 CC thyroid cancers, etc.  
 SQ Sequence 947 BP; 207 A; 271 C; 273 G; 196 T;

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seq\_documentation\_block:

ID T72311 standard; cDNA; 947 BP.



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gene, exon 2 and partial cds.
ACCESSION U79633
VERSION U79633.1 GI:4098147
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A. and Fernandez-Piqueras, J.
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
JOURNAL Unpublished
REFERENCE
AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A. and Fernandez-Piqueras, J.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
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TITLE Direct Submission  
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,  
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DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))  
gene, exon 2 and partial cds.  
ACCESSION U79632

U79632.1 GI:4098151  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1 (bases 1 to 339)  
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,  
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.  
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains  
Unpublished  
JOURNAL 2 (bases 1 to 339)  
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,  
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.  
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 ; Patent No. 5843756  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stone, Steven  
 ; APPLICANT: Jlang, Ping  
 ; APPLICANT: Kamb, Alexander  
 ; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
 ; NUMBER OF SEQUENCES: 47  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 ; STREET: 1201 New York Avenue, Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/508,735  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US to be assigned  
 ; FILING DATE: 07-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/03316  
 ; FILING DATE: 17-MAR-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Inhen, Jeffrey L.  
 ; REGISTRATION NUMBER: 28,957  
 ; REFERENCES/DOCKET NUMBER: 24884-109348  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-962-4848  
 ; TELEFAX: 202-962-8300  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 507 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
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 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
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seq_documentation_block:
; Sequence 1, Application US/08534975
; Patent No. 5723313
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 5723313el Regulator of the Mammalian Cell
; TITLE OF INVENTION: Cycle
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,975
; FILING DATE: 28-SEP-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0590000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
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; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 5876965el Regulator of the
; TITLE OF INVENTION: Mammalian Cell Cycle
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
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; COMPUTER READABLE FORM:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,470
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/534,975
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0590000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
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; Patent No. 6046032
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 6046032el Regulator of the Mammalian
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue Sule 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/954,470
; FILING DATE: 20-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/534,975
; FILING DATE: 27-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-023 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: unknown
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; Sequence 5, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
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; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
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; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
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; Sequence 5, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,274
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117 FILING DATE: 15-JULY-1997
118 CLASSIFICATION: 800
119 PRIOR APPLICATION DATA:
120 FILING DATE: 14-SEPTEMBER-1994
121 PRIOR APPLICATION NUMBER: US 08/306,511
122 FILING DATE: 14-SEPTEMBER-1994
123 PRIOR APPLICATION DATA:
124 FILING DATE: 23-MAY-1994
125 PRIOR APPLICATION NUMBER: US 08/248,812
126 FILING DATE: 23-MAY-1994
127 PRIOR APPLICATION DATA:
128 FILING DATE: 14-APRIL-1994
129 PRIOR APPLICATION NUMBER: US 08/227,371
130 FILING DATE: 18-NOVEMBER-1993
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132 FILING DATE: 18-NOVEMBER-1993
133 PRIOR APPLICATION NUMBER: US 07/991,997
134 FILING DATE: 17-DECEMBER-1992
135 PRIOR APPLICATION DATA:
136 FILING DATE: 07/963,308
137 PRIOR APPLICATION NUMBER: US 07/963,308
138 FILING DATE: 16-OCTOBER-1992
139 ATTORNEY/AGENT INFORMATION:
140 NAME: Vincent, Matthew P.
141 REGISTRATION NUMBER: 36,709
142 REFERENCE/DOCKET NUMBER: MIV-071.09
143 TELECOMMUNICATION INFORMATION:
144 TELEPHONE: (617) 832-1000
145 TELEFAX: (617) 832-7000
146 INFORMATION FOR SEQ ID NO: 5:
147 SEQUENCE CHARACTERISTICS:
148 LENGTH: 853 base pairs
149 TYPE: nucleic acid
150 STRANDEDNESS: both
151 TOPOLOGY: linear
152 MOLECULE TYPE: cDNA
153 FEATURE:
154 NAME/KEY: CDS
155 LOCATION: 213..587
156 US-08-893-274-5

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157 Quality: 658.00 Length: 125
158 Ratio: 5.264 Gaps: 0
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181 ; Patent No. 6043030
182 ; GENERAL INFORMATION:
183 ; APPLICANT: Beach, David H.
184 ; APPLICANT: Demetrick, Douglas J.
185 ; APPLICANT: Serrano, Manuel
186 ; APPLICANT: Hannon, Gregory J.
187 ; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
188 ; NUMBER OF SEQUENCES: 39
189 ; CORRESPONDENCE ADDRESS:
190 ; ADDRESSEE: Foley, Hoag & Elliot
191 ; STREET: One Post Office Square
192 ; CITY: Boston
193 ; STATE: MA
194 ; COUNTRY: USA
195 ; ZIP: 02109
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202 ; APPLICATION NUMBER: US/08/581,918A
203 ; FILING DATE: 02-JAN-1996
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207 ; FILING DATE: 30-JUN-1995
208 ; PRIOR APPLICATION DATA:
209 ; APPLICATION NUMBER: US 08/346,147
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211 ; PRIOR APPLICATION DATA:
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213 ; FILING DATE: 14-SEP-1994
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215 ; APPLICATION NUMBER: US 08/248,812
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221 ; APPLICATION NUMBER: US 08/154,915
222 ; FILING DATE: 18-NOV-1993
223 ; PRIOR APPLICATION DATA:
224 ; APPLICATION NUMBER: US 07/991,997
225 ; FILING DATE: 17-DEC-1992
226 ; ATTORNEY/AGENT INFORMATION:
227 ; NAME: Vincent, Matthew P.
228 ; REGISTRATION NUMBER: 36,709
229 ; REFERENCE/DOCKET NUMBER: MIV-071.06
230 ; TELECOMMUNICATION INFORMATION:
231 ; TELEPHONE: (617) 832-1299
232 ; TELEFAX: (617) 832-7000
233 ; INFORMATION FOR SEQ ID NO: 5:
234 ; SEQUENCE CHARACTERISTICS:
235 ; LENGTH: 853 base pairs
236 ; TYPE: nucleic acid
237 ; STRANDEDNESS: both
238 ; TOPOLOGY: linear
239 ; MOLECULE TYPE: cDNA
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
; LOCATION: 213..587
; PCT-US95-04636-5

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; Sequence 5, Application US/08627610
; Patent No. 5919997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 857 base pairs
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; Sequence 25, Application US/08474177
; Patent No. 5624819
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 base pairs
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; STRANDEDNESS: double
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; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
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; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
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; FILING DATE: 01-JUN-1994
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; FILING DATE: 18-MAR-1994
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; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
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; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
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; LENGTH: 395 base pairs
; TYPE: nucleic acid
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; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
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; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
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; LENGTH: 395 base pairs
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; TOPOLOGY: linear
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; ANTI-SENSE: NO
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; FILING DATE: 17-MAR-1995
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; FILING DATE: 01-JUN-1994
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; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
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; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227.369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214.582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
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; TELEFAX: 202-962-8300
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; Sequence 25, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
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; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
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; TYPE: nucleic acid
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; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,251
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/474,083
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
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; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
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; ANTI-SENSE: NO
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; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; PRIOR APPLICATION DATA:
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FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 25:  
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LENGTH: 395 base pairs  
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STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-486-047-25

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Ratio: 5.235 Gaps: 0  
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 Copyright (c) 1993-2000 Compugen Ltd.

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 (CGAP/BTCAP), Tumor Gene Index  
 Unpublished (1998)  
 On Oct 30, 1998 this sequence version replaced gi:3813427.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
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 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Tel.: (301) 496-1550  
 Email: [Robert\\_Strausberg@nih.gov](mailto:Robert_Strausberg@nih.gov)  
 Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
 M.D., Louis M. Staudt, M.D., Ph.D.





Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
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 BASE COUNT 113 a 158 c 177 g 130 t 1 others  
 ORIGIN

alignment\_scores:  
 Quality: 315.00 Length: 122  
 Ratio: 3.351 Gaps: 2  
 Percent Similarity: 77.049 Percent Identity: 55.738

# alignment\_block:

US-09-016-869A-6 x A1198233/rev ..

Align seg 1/1 to reverse of: A1198233 from: 1 to: 579

1 MetMetMetGlyAsnValHisValAlaLeuLeuLeuAsnTyrGlyAl 17  
 |||||.....:||||| |||||.....:|||||  
 549 ATGATGATGGCGAGCGCGAGTGGCGAAGCTGCTGCTCCACAGCG 500  
 |||||.....:||||| |||||.....:|||||  
 17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34  
 |||||.....:||||| |||||.....:|||||  
 499 GAAGCCCACTGGCGCGCGCGCCACTCTACCCGACCCGTCGACGAGC 450  
 |||||.....:||||| |||||.....:|||||  
 34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50  
 |||||.....:||||| |||||.....:|||||  
 449 CTGCCCGGAGGGCTTCCTGGACACGCTGGTGTGTGCACCGGGCGG 400  
 |||||.....:||||| |||||.....:|||||  
 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67  
 |||||.....:||||| |||||.....:|||||  
 399 GCGCGCTGGACGTGGCGATGCTGCGGCGCTGCTGCGGACCTGGC 350  
 |||||.....:||||| |||||.....:|||||  
 67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84  
 |||||.....:||||| |||||.....:|||||  
 349 TGAGAGCTGGCGCATCGCGATGTCGACGGTACCTGCGCGGGCT... 304  
 |||||.....:||||| |||||.....:|||||  
 84 ySerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100  
 |||||.....:||||| |||||.....:|||||  
 303 .....GCGGGGGGACCC.....AGGGCAGTACCATGCC 274  
 |||||.....:||||| |||||.....:|||||  
 101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117  
 ::|||::: |||||.....:|||||  
 273 CGCATAGATGCGCGGAAGGTCCCTCAGACATCCCGGATTGAAGAACC 224  
 |||||.....:||||| |||||.....:|||||  
 117 uArgGlyGlnSerGln 122  
 |||||.....:|||||

223 GAGAGGCTGTGAGAA 208

seq\_name: gb\_gss7:AQ496105

seq\_documentation\_block: 614 bp DNA GSS 28-APR-1999

LOCUS AQ496105 HS\_5075\_Al\_F12\_T7 RPCI-11 Human Male BAC Library Homo sapiens  
 DEFINITION genomic clone Plate-651 Col-23 Row-K, genomic survey sequence.  
 ACCESSION AQ496105

VERSION AQ496105.1 GI:4696228

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 614)  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE 93380589

COMMENT On Dec 15, 1999 this sequence version replaced gi:4575297.

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallaceu.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htseq.washington.edu>

Plate: 651 row: K column: 23

Seq primer: T7

Class: BAC ends

High quality sequence stop: 614.

# FEATURES

source  
 Location/Qualifiers  
 1. .614  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-651 Col-23 Row-K"  
 /clone.lib="RPCI-11 Human Male BAC Library"  
 /sex="male"  
 /note="vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 117 a 182 c 171 g 133 t 11 others  
 ORIGIN

# alignment\_scores:

Quality: 312.00 Length: 81  
 Ratio: 4.274 Gaps: 0  
 Percent Similarity: 90.123 Percent Identity: 72.840

# alignment\_block:

US-09-016-869A-6 x AQ496105 ..

Align seg 1/1 to: AQ496105 from: 1 to: 614

1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuAsnTyrGlyAl 17  
 |||||.....:||||| |||||.....:|||||  
 297 ATGATGATGGCGACCGCGAGTGGCGGAGCTGCTGCTCCACGGGCG 346  
 |||||.....:||||| |||||.....:|||||  
 17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34

```

1::: ||||| - |||||:::|||||:::|||||:::|||||
347 GGAGCCCACTGGCGGACCCGCCACTCTACCCGACCGTGCACGACG 396
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||:::|||||:::|||||:::|||||:::|||||
397 CTGCGCGGAGGCTTCTCTGGACACACTGGTGTGCTGCACCGGCGGG 446
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
|||||:::|||||:::|||||:::|||||:::|||||
447 GCGCGGCTGACGTCGCTATGCTGGGCGCGTCTGCCGTGGACCTGCG 496
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSer 81
|||||:::|||||:::|||||:::|||||:::|||||
497 TGAGGAGCTGGGCGCATCTCGATGTTACACGGTACCTGCGCGCG 539

```

seq\_name: gb\_est25:AI765096

seq\_documentation\_block: 774 bp mRNA EST 21-DEC-1999  
 LOCUS AI765096  
 DEFINITION w148b08.x1 NCI\_CGAP\_Col16 Homo sapiens cDNA clone IMAGE:2393463 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;contains LTR9.b3 MER22 repetitive element ;, mRNA sequence.

ACCESSION AI765096  
 VERSION AI765096.1 GI:5231605

KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 774)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On Feb 22, 1999 this sequence version replaced gi:4283180.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,

M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 854 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 400.

Location/Qualifiers

FEATURES

source

```

1..774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI_CGAP_Col16"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1; Not 1; Site: 2; Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col16 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo."
153 a 220 c 221 g 179 t 1 others

```

BASE COUNT  
 ORIGIN

alignment\_scores:

Quality: 312.00

Ratio: 3.429

Length: 120

Gaps: 3.

Percent Similarity: 75.833 Percent Identity: 57.500

alignment\_block:

US-09-016-869A-6 x AI765096/rev ..

Align seg 1/1 to reverse of: AI765096 from: 1 to: 774

1 MetMetMetGlyAsnValHisValAlaLeuLeuLeuAsnTyrGlyAl 17  
 |||||:::|||||:::|||||:::|||||:::|||||

584 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGCGC 535

17 aspSerAsnCysGluaspProThrThrPheSerArgProValHisasp 34  
 |||||:::|||||:::|||||:::|||||:::|||||

534 GGAGCCCAATTGGGCGCGACCCCGCCACTTTCACCCGAACCGTGCACGACG 485

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50  
 |||||:::|||||:::|||||:::|||||:::|||||

484 CTGCGCGGAGGGGCTTCTGGACACGCTGGTGTGCTGCACCGGCGCGG 435

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67  
 |||||:::|||||:::|||||:::|||||:::|||||

434 GCGCGGCTGGACGTGCGCAATGCTGGGCGCGTCTGCCGTGGACCTGGC 385

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84  
 |||||:::|||||:::|||||:::|||||:::|||||

384 TGAGGAGCTGGGCGCATCGCATGTGCGCGCGGTACCTGCGCGCGGCT... 339

84 ysSerLeuCySerAlaGlyTrpSerLeuCyThrAlaGly...AsnVal 99  
 |||||:::|||||:::|||||:::|||||:::|||||

338 .....TCGGGGGGC.....ACCAGAGCGAGTAACCAT 312

100 AlaGlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGl 116  
 |||||:::|||||:::|||||:::|||||:::|||||

311 GCGCGCATAAATGCGGGAAGGTCCCTCAGACATCCCGCATTTAAAGAA 262

116 uLeuArgGly 119

261 CCAAGAGGG 252

seq\_name: gb\_est19:AI362049

seq\_documentation\_block: 580 bp mRNA EST 15-FEB-1999

LOCUS AI362049

DEFINITION qy39f07.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ;, mRNA sequence.

ACCESSION AI362049

VERSION AI362049.1 GI:4113670

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 580)

AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 884 Std Error: 0.00

Seq primer: -40UP from Gibco









14:40 2000

545 ATGATGATGGCCAGCGCCGAGTGGCGGAGTGTGCTGCTCCACGGCG 496  
17 aasSerAsnCysGluAspProThrPheSerArgProValHisAspA 34  
495 GGAGCCCAACTG.CCCGACCCGCAACTCTCACCCAGCCGTCACGACG 447  
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50  
446 CTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGTCACCGCGCGG 397  
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67  
396 GCAGCGCTGGACGTCGGGATGCGTGGGGCGCTGCTGCCCGTGGACCTGGC 347  
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84  
346 TGAGGAGCTGGCCATCGCGATGTGCGACGCTGCTGCTGCTGCGCGCGCT... 301  
84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100  
300 .....CGCGGGGGCGACCC.....AGAGGCGAGTACCATGCC 271  
101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117  
270 CGCATAGATGCGCGGAGTCCCTCAGACATCCCGGATTGAAGAAGCA 221  
117 uArgGlyGlnSerGln 122  
220 GAGAGGCTCTGAGAAA 205  
seq\_name: gb\_est13:AA909181  
seq\_documentation\_block: 526 bp mRNA EST 10-JUN-1998  
LOCUS AA909181  
DEFINITION IMAGE:1523215 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE  
REGULATOR BETA FORM ; mRNA sequence.  
ACCESSION AA909181  
VERSION AA909181.1 GI:3048586  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Apr 7, 1998 this sequence version replaced gi:3034533.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 581 Std Error: 0.00  
Seq primer: -40m13 fwd. ER from Amersham  
High quality sequence stop: 398.  
Location/Qualifiers  
1. 526  
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/clone="IMAGE:1523215"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site: 1: Not 1; Site: 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI-CGAP-GCB1) were mixed, and ss circles were used as  
tracer. Following HAP purification, this DNA was used as  
was PCR-amplified cDNAs from pools of 5,000 clones made

108 SerSerThrProArgAlaLeuGluLeuArgGlyGlnSerGln 122  
3CACC.....AGAGGAGTAACCATGCGCGATAGATGCCCGGAAGGT 253  
252 CCCTCAGACATCCCGATGAAGAACAGAGAGGCTCTGAGAAA 208  
seq\_name: gb\_est27:AI954684  
seq\_documentation\_block: 563 bp mRNA EST 08-MAR-2000  
LOCUS AI954684  
DEFINITION wq34h12.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2473223 3',  
similar to SW:CDN2\_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR  
A ; mRNA sequence.  
ACCESSION AI954684  
VERSION AI954684.1 GI:5746994  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 563)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
CDNA sequencing by: Washington University Genome Sequencing Center  
CDNA distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/brp/image/image.html  
Insert Length: 613 from Glibco  
Seq primer: -400P from Glibco  
High quality sequence stop: 460.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:2473223"  
/clone\_lib="NCI-CGAP-GC6"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Plasmid DNA from the normalized library  
NCI-CGAP-GC4 was prepared, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (clonids 1257096-1258631,  
1469064-1470983, and 1475592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldo.  
112 a 158 c 169 g 124 t  
BASE COUNT  
ORIGIN  
alignment\_scores:  
Quality: 299.00 Length: 122  
Ratio: 3.101 Gaps: 2  
Percent Similarity: 77.049 Percent Identity: 56.557  
alignment\_block:  
US-09-016-869A-6 x AI954684/rev ..  
Align seg 1/1 to reverse of: AI954684 from: 1 to: 563  
1 MetMetGlyAsnValHisValAlaLeuLeuLeuAsnTyrGlyAl 17  
|||||



